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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:44 ; Search time 18 Seconds
(without alignments)
998.102 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSDVSLIFLM.....ITBSKDMHFFSLGCIILDLV 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
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3: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1800	100.0	348	4 US-09-009-893A-6	Sequence 6, Appli
2	1800	100.0	348	4 US-09-489-155-6	Sequence 6, Appli
3	1635	90.8	480	3 US-08-795-088A-2	Sequence 2, Appli
4	1635	90.8	480	4 US-09-009-893A-2	Sequence 2, Appli
5	1635	90.8	480	4 US-09-489-155-2	Sequence 2, Appli
6	1579	87.7	480	4 US-09-069-023-34	Sequence 34, Appli
7	1554.5	86.4	445	3 US-08-859-167-2	Sequence 2, Appli
8	1554.5	86.4	445	3 US-09-109-273-2	Sequence 2, Appli
9	1554.5	86.4	445	3 US-09-276-993-2	Sequence 2, Appli
10	1554.5	86.4	445	4 US-09-723-450-2	Sequence 2, Appli
11	527	29.3	221	3 US-09-382-155-17	Sequence 17, Appli
12	527	29.3	221	3 US-09-074-044A-17	Sequence 2, Appli
13	363	21.3	84	3 US-09-382-155-2	Sequence 2, Appli
14	363	20.5	84	3 US-09-382-155-2	Sequence 2, Appli
15	313	17.4	479	4 US-08-983-502-7	Sequence 7, Appli
16	313	17.4	479	4 US-08-516-747-7	Sequence 7, Appli
17	313	17.4	479	5 PCT-US96-10521-7	Sequence 7, Appli
18	311.5	17.3	478	4 US-09-009-893A-3	Sequence 3, Appli
19	311.5	17.3	478	4 US-09-489-155-3	Sequence 3, Appli
20	311	17.3	479	2 US-08-807-200-12	Sequence 12, Appli
21	311	17.3	479	2 US-09-382-155-28	Sequence 28, Appli
22	311	17.3	479	3 US-09-001-777-12	Sequence 12, Appli
23	311	17.3	479	3 US-09-074-044A-26	Sequence 26, Appli
24	311	17.3	479	3 US-09-074-044A-27	Sequence 27, Appli
25	311	17.3	479	3 US-09-074-044A-28	Sequence 28, Appli
26	309	17.2	479	3 US-08-852-782-3	Sequence 3, Appli
27	306	17.0	479	3 US-09-382-155-27	Sequence 27, Appli

28	304.5	16.9	464	4 US-08-983-502-18	Sequence 18, Appli
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30	304.5	16.9	464	4 PCT-US96-10521-18	Sequence 18, Appli
31	303	16.8	479	3 US-09-382-155-26	Sequence 26, Appli
32	302.5	16.8	389	1 US-08-618-408B-4	Sequence 4, Appli
33	302.5	16.8	496	1 US-08-665-220-4	Sequence 4, Appli
34	302.5	16.8	496	1 US-09-291-692-4	Sequence 2, Appli
35	296.5	16.5	476	4 US-09-561-756-27	Sequence 27, Appli
36	296.5	16.5	476	4 US-09-227-721-27	Sequence 27, Appli
37	296.5	16.5	476	4 US-09-954-697-27	Sequence 27, Appli
38	261.5	14.5	335	4 US-08-983-502-16	Sequence 16, Appli
39	261.5	14.5	335	4 US-09-516-747-16	Sequence 16, Appli
40	261.5	14.5	335	5 PCT-US96-10521-16	Sequence 16, Appli
41	248.5	13.8	521	4 US-09-952-834A-2	Sequence 2, Appli
42	244	13.6	479	1 US-09-665-220-2	Sequence 2, Appli
43	244	13.6	479	3 US-09-291-692-2	Sequence 2, Appli
44	244	13.6	479	3 US-09-561-756-33	Sequence 33, Appli
45	244	13.6	479	4 US-09-227-721-33	Sequence 33, Appli

ALIGNMENTS

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RESULT 1
US-09-009-893A-6
; Sequence / Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION
; APPLICANT: M. Chan
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner U.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-009-893A-6
Query Match 100.0%; Score 1800; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.1e-183; Indels 0; Gaps 0;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MAEIGEDLDKSDVSLIFLMKDYMGKTSKESKSPFLDVLVELEKINLVAPDQDLLEKCL 60
Db 1 MAEIGEDLDKSDVSLIFLMKDYMGKTSKESKSPFLDVLVELEKINLVAPDQDLLEKCL 60
Cy 61 KNHRIIDLKTIKIQKOSVOGAGTSYRNVLOAAIQKSLKDPNNRREPVKKSIOSENAF 120
Db 61 KNHRIIDLKTIKIQKOSVOGAGTSYRNVLOAAIQKSLKDPNNRREPVKKSIOSENAF 120
Cy 61 KNHRIIDLKTIKIQKOSVOGAGTSYRNVLOAAIQKSLKDPNNRREPVKKSIOSENAF 120
Db 61 KNHRIIDLKTIKIQKOSVOGAGTSYRNVLOAAIQKSLKDPNNRREPVKKSIOSENAF 120
Cy 121 LPOSIPERRYKMSKPLGICLIIDICIGNETELLRDPFTSLGYEVOKFLTSMHGISOILG 180
Db 121 LPOSIPERRYKMSKPLGICLIIDICIGNETELLRDPFTSLGYEVOKFLTSMHGISOILG 180
Cy 121 LPOSIPERRYKMSKPLGICLIIDICIGNETELLRDPFTSLGYEVOKFLTSMHGISOILG 180
Db 121 LPOSIPERRYKMSKPLGICLIIDICIGNETELLRDPFTSLGYEVOKFLTSMHGISOILG 180
Cy 181 QPACMPHRDYDSFVCLVSRGSGSVYGVDTGHSGLPLHRIKRVFMGDCPYLAGKPKM 240
Db 181 QPACMPHRDYDSFVCLVSRGSGSVYGVDTGHSGLPLHRIKRVFMGDCPYLAGKPKM 240
Cy 241 FFITNYVYSGQLEDLSLELVDPGPAKNTVEPKAKRGKGLCTVAREADFFESLCTADMSLLE 300
Db 241 FFITNYVYSGQLEDLSLELVDPGPAKNTVEPKAKRGKGLCTVAREADFFESLCTADMSLLE 300
Cy 241 FFITNYVYSGQLEDLSLELVDPGPAKNTVEPKAKRGKGLCTVAREADFFESLCTADMSLLE 300
Db 241 FFITNYVYSGQLEDLSLELVDPGPAKNTVEPKAKRGKGLCTVAREADFFESLCTADMSLLE 300
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Wed Sep 8 06:14:12 2004

us-10-713-208-6.open.ra1

Page 2

QY 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348
DB 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348

RESULT 2
US-09-489-155-6
Sequence 5, Application US/09489155
Patent No. 6680171
GENERAL INFORMATION
APPLICANT: NI, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner J.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
FILE REFERENCE: 1488.097002
CURRENT APPLICATION NUMBER: US/09/489,155
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/009,893
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: US 60/034,205
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent version 3.0
SEQ ID NO 6
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-09-489-155-6

Query Match 100.0%; Score 1800; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.1e-183;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKEKSFLLDIYVELEKLNVAPODLLEKCL 60
DB 1 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKEKSFLLDIYVELEKLNVAPODLLEKCL 60
QY 61 KNIRIDLTXTKIQKTKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEPVKKSIOESBAF 120
DB 61 KNIRIDLTXTKIQKTKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEPVKKSIOESBAF 120
QY 121 LPOSIPEERYKMSKPIGLICLLIDCIGNETELRLRFTSLGVEVQKFLHLSMHGISQILG 180
DB 121 LPOSIPEERYKMSKPIGLICLLIDCIGNETELRLRFTSLGVEVQKFLHLSMHGISQILG 180
QY 181 QFACMPHRDYDSFVCLVSRGSSQSVYGVDTSGPLPHIRRMFMGDSQCYLAGKXPM 240
DB 181 QFACMPHRDYDSFVCLVSRGSSQSVYGVDTSGPLPHIRRMFMGDSQCYLAGKXPM 240
QY 241 FFIONVYVSDQCLFDSLSLEVDGPANKNVEFKAQKRGCLCTVAREADFTWGLCTADMSILE 300
DB 241 FFIONVYVSDQCLFDSLSLEVDGPANKNVEFKAQKRGCLCTVAREADFTWGLCTADMSILE 300
QY 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348
DB 301 QSHSPSLYLQCLSQKLRQERTIPGSGITSEKDMHFSGLCILLDVL 348

RESULT 3
US-08-795-088A-2
Sequence 2, Application US/08795088A
Patent No. 6242569
GENERAL INFORMATION
APPLICANT: NI, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner J.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor R
FILE REFERENCE: 1488.097002
CURRENT APPLICATION NUMBER: US/09/009,893A

STREET: 75 Denise Drive
CITY: Hillsborough
STATE: California
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,088A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4342
TELEFAX: (650) 343-4341
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-795-088A-2

Query Match 90.8%; Score 1635; DB 3; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.8e-166;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
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DB 97 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKEKSFLLDIYVELEKLNVAPODLLEKCL 156
QY 61 KNIRIDLTXTKIQKTKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEPVKKSIOESBAF 120
DB 157 KNIRIDLTXTKIQKTKQSVQAGTSYRNVLQAAIQKSLKDPNNFEEPVKKSIOESBAF 106
QY 107 ----EEPVKKSIOESBAFIPSIPEERYKMSKPIGLICLLIDCIGNETELRLRFTSLGY 162
DB 217 LGAQDPEPVKKSIOESBAFIPSIPEERYKMSKPIGLICLLIDCIGNETELRLRFTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCLVSRGSSQSVYGVDTSGPLPHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPHRDYDSFVCLVSRGSSQSVYGVDTSGPLPHI 336
QY 223 RRMFMGDSQCYLAGKXPMFFIONVYVSDQCLFDSLSLEVDGPANKNVEFKAQKRGCLCTV 282
DB 337 RRMFMGDSQCYLAGKXPMFFIONVYVSDQCLFDSLSLEVDGPANKNVEFKAQKRGCLCTV 396
QY 283 READPFWGLCTADMSILEQSHSPSLYLQCLSQKLRQER 321
DB 397 READPFWGLCTADMSILEQSHSPSLYLQCLSQKLRQER 435

RESULT 4
US-09-009-893A-2
Sequence 2, Application US/09009893A
Patent No. 623938
GENERAL INFORMATION
APPLICANT: NI, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner J.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor R
FILE REFERENCE: 1488.097002
CURRENT APPLICATION NUMBER: US/09/009,893A

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/ CURRENT FILING DATE: 1998-02-21
/ PRIOR APPLICATION NUMBER: US 60/054,800
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: US 60/034,205
/ PRIOR FILING DATE: 1997-01-21
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-009-893A-2

Query Match      90.8%; Score 1635; DB 4; Length 480;
Best Local Similarity 94.1%; Pred. No. 7,8e-16e;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKSFLLDVELEKLNVAPODLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKSFLLDVELEKLNVAPODLLEKCL 156
QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 106
DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 216
QY 107 ----EEPVKKSIOSESAFLPQSIPEERYKMKSKPGLICIIDICGNETELLADPTFSLGY 162
DB 217 LGAQOEVPKKSIOSESAFLPQSIPEERYKMKSKPGLICIIDICGNETELLADPTFSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLHHI 336
QY 223 RRMFMGDSCEPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVBFKQKGLCTVH 282
DB 337 RRMFMGDSCEPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVBFKQKGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXLRQER 435

RESULT 5
US-09-489-155-2
/ Sequence 2, Application US/09489155
/ Patent No. 6680171
/ GENERAL INFORMATION:
/ APPLICANT: N1, Jiah
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Dixit, Vishva M.
/ APPLICANT: Gentz, Reiner L.
/ APPLICANT: Kenny, Joseph J.
/ TITLE OF INVENTION: I-FLICE A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
/ TITLE OF INVENTION: CD-95 Induced Apoptosis
/ FILE REFERENCE: 1488.0970002
/ CURRENT APPLICATION NUMBER: US/09/489,155
/ CURRENT FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 09/009,893
/ PRIOR FILING DATE: 1998-01-21
/ PRIOR APPLICATION NUMBER: US 60/034,205
/ PRIOR FILING DATE: 1997-01-21
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-489-155-2

Query Match      90.8%; Score 1635; DB 4; Length 480;
Best Local Similarity 94.1%; Pred. No. 7,8e-16e;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

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DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKSFLLDVELEKLNVAPODLLEKCL 156
QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 106
DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 216
QY 107 ----EEPVKKSIOSESAFLPQSIPEERYKMKSKPGLICIIDICGNETELLADPTFSLGY 162
DB 217 LGAQOEVPKKSIOSESAFLPQSIPEERYKMKSKPGLICIIDICGNETELLADPTFSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLHHI 336
QY 223 RRMFMGDSCEPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVBFKQKGLCTVH 282
DB 337 RRMFMGDSCEPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVBFKQKGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXLRQER 435

RESULT 6
US-09-069-023-34
/ Sequence 34, Application US/09069023A
/ Patent No. 634573
/ GENERAL INFORMATION:
/ APPLICANT: Nunez, Gabriel
/ APPLICANT: Inohara, Naohiro
/ APPLICANT: Koseki, Takeyoshi
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
/ TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
/ FILE REFERENCE: UM-03333
/ CURRENT APPLICATION NUMBER: US/09/069,023A
/ CURRENT FILING DATE: 1998-04-27
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 34
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-069-023-34

Query Match      87.7%; Score 1579; DB 4; Length 480;
Best Local Similarity 91.2%; Pred. No. 7,5e-16e;
Matches 309; Conservative 4; Mismatches 8; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKSFLLDVELEKLNVAPODLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKSKSKSFLLDVELEKLNVAPODLLEKCL 156
QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 106
DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIOKSLKDPNNFR----- 216
QY 107 ----EEPVKKSIOSESAFLPQSIPEERYKMKSKPGLICIIDICGNETELLADPTFSLGY 162
DB 217 LGAQOEVPKKSIOSESAFLPQSIPEERYKMKSKPGLICIIDICGNETELLADPTFSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPBEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLHHI 336
QY 223 RRMFMGDSCEPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVBFKQKGLCTVH 282
DB 337 RRMFMGDSCEPYLAGKPKMFFIQNYVVSQGLSDLSLEVDGPMKNVBFKQKGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSOXLRQER 435

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RESULT 7
US-08-859-167-2
Sequence 2, Application US/08859167
Patent No. 6037461
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461, is
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,167
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-859-167-2

Query Match 86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 2.8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFMKDYMGKGIKSKSFIDLVELEKLNVAPODLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFMKDYMGKGIKSKSFIDLVELEKLNVAPODLDLEKCL 156
QY 61 KNHRIIDLTKIÖKRYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFREPEPVKKSIOESEAF 120
DB 157 KNHRIIDLTKIÖKRYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFREPEPVKKSIOESEAF 202
QY 121 LPOSIPEERYKMKSKPLGICLIIDICIGNETELRDTFTSLGVEVÖKFLHLSMHGISOILG 180
DB 203 --SIPERYKMKSKPLGICLIIDICIGNETELRDTFTSLGVEVÖKFLHLSMHGISOILG 259
QY 181 ÖFACMEPHRDYDSVFCVLVSRGSGSVYGVÖTHSGPLPHIIRRMFMGDSCPYLAGKPKM 240
DB 260 ÖFACMEPHRDYDSVFCVLVSRGSGSVYGVÖTHSGPLPHIIRRMFMGDSCPYLAGKPKM 319
QY 241 FFIÖNYVSDGÖLESDSLLEVDPAMKAVEFKÖKRGCLCTVHREADPFWSICTADMSLLE 300
DB 320 FFIÖNYVSDGÖLESDSLLEVDPAMKAVEFKÖKRGCLCTVHREADPFWSICTADMSLLE 379
QY 301 ÖSHSPSLYLOCTLSÖKLRÖER 321
DB 380 ÖSHSPSLYLOCTLSÖKLRÖER 400

RESULT 8
US-09-109-273-2
Sequence 2, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760, is
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-109-273-2

Query Match 86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 2.8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFMKDYMGKGIKSKSFIDLVELEKLNVAPODLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFMKDYMGKGIKSKSFIDLVELEKLNVAPODLDLEKCL 156
QY 61 KNHRIIDLTKIÖKRYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFREPEPVKKSIOESEAF 120
DB 157 KNHRIIDLTKIÖKRYKQSVÖGAGTSYRNVLÖAIÖKSLKDPNNFREPEPVKKSIOESEAF 202
QY 121 LPOSIPEERYKMKSKPLGICLIIDICIGNETELRDTFTSLGVEVÖKFLHLSMHGISOILG 180
DB 203 --SIPERYKMKSKPLGICLIIDICIGNETELRDTFTSLGVEVÖKFLHLSMHGISOILG 259
QY 181 ÖFACMEPHRDYDSVFCVLVSRGSGSVYGVÖTHSGPLPHIIRRMFMGDSCPYLAGKPKM 240
DB 260 ÖFACMEPHRDYDSVFCVLVSRGSGSVYGVÖTHSGPLPHIIRRMFMGDSCPYLAGKPKM 319
QY 241 FFIÖNYVSDGÖLESDSLLEVDPAMKAVEFKÖKRGCLCTVHREADPFWSICTADMSLLE 300
DB 320 FFIÖNYVSDGÖLESDSLLEVDPAMKAVEFKÖKRGCLCTVHREADPFWSICTADMSLLE 379
QY 301 ÖSHSPSLYLOCTLSÖKLRÖER 321
DB 380 ÖSHSPSLYLOCTLSÖKLRÖER 400


```
RESULT 9
US-09-276-993-2
; Sequence 2, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801xis
; STREET: One Liberty Place, 46th floor
; City: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeJuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3438
; TELEFAX: (215) 568-3438
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-276-993-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 2,8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSILFLMKDYNGRGKISKESFLDLVLEKLNLAAPQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSILFLMKDYNGRGKISKESFLDLVLEKLNLAAPQDLLEKCL 156
QY 61 KNHRIDLTKTKIQKXKQSYOGAGTSYRNVLQAAIQKSLKDPNNRREBPVKKSIQESSAF 120
DB 157 KNHRIDLTKTKIQKXKQSYOGAGTSYRNVLQAAIQKSLKDPNNR----- 202
QY 121 LPSGIPERRYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSWHSISQILG 180
DB 203 ---SIPERRYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSWHSISQILG 259
QY 181 QFACMPERRDYDFVCLVLSRSGSQSYGVDPQTHSGPLPHIRRMFMGDSCEYLAKGPKM 240
DB 260 QFACMPERRDYDFVCLVLSRSGSQSYGVDPQTHSGPLPHIRRMFMGDSCEYLAKGPKM 319
QY 241 FFIQNYVSDGQLEDSSILLEVDPGPMKNVEFKAQKRGCLCTVREADPFWSLCTADMSLLE 300
DB 320 FFIQNYVSDGQLEDSSILLEVDPGPMKNVEFKAQKRGCLCTVREADPFWSLCTADMSLLE 379
QY 301 QSHSSPSLYIQCLSQKLRQER 321
DB 380 QSHSSPSLYIQCLSQKLRQER 400
```

```
RESULT 10
US-09-723-450-2
; Sequence 2, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: T012445
; CURRENT APPLICATION NUMBER: US/09/723,450
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576751e1 Sequence
; US-09-723-450-2

Query Match      86.4%; Score 1554.5; DB 4; Length 445;
Best Local Similarity 94.4%; Pred. No. 2,8e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSILFLMKDYNGRGKISKESFLDLVLEKLNLAAPQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSILFLMKDYNGRGKISKESFLDLVLEKLNLAAPQDLLEKCL 156
QY 61 KNHRIDLTKTKIQKXKQSYOGAGTSYRNVLQAAIQKSLKDPNNRREBPVKKSIQESSAF 120
DB 157 KNHRIDLTKTKIQKXKQSYOGAGTSYRNVLQAAIQKSLKDPNNR----- 202
QY 121 LPSGIPERRYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSWHSISQILG 180
DB 203 ---SIPERRYKMKSPKLGICLIIDICGNETELLRDTFTSLGYEVQKFLHSWHSISQILG 259
QY 181 QFACMPERRDYDFVCLVLSRSGSQSYGVDPQTHSGPLPHIRRMFMGDSCEYLAKGPKM 240
DB 260 QFACMPERRDYDFVCLVLSRSGSQSYGVDPQTHSGPLPHIRRMFMGDSCEYLAKGPKM 319
QY 241 FFIQNYVSDGQLEDSSILLEVDPGPMKNVEFKAQKRGCLCTVREADPFWSLCTADMSLLE 300
DB 320 FFIQNYVSDGQLEDSSILLEVDPGPMKNVEFKAQKRGCLCTVREADPFWSLCTADMSLLE 379
QY 301 QSHSSPSLYIQCLSQKLRQER 321
DB 380 QSHSSPSLYIQCLSQKLRQER 400

RESULT 11
US-09-382-155-17
; Sequence 17, Application US/09382155B
; Patent No. 6160895
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; PRIOR FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
```

SEQ ID NO 17
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-17

Query Match 29.3%; Score 527; DB 3; Length 221;
Best Local Similarity 100.0%; Pred. No. 5.5e-48;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 156
QY 61 KNHRIIDLKTKIQKQKQSVQAGTSYRNVLAALQKSLKDPNNFR 106
DB 157 KNHRIIDLKTKIQKQKQSVQAGTSYRNVLAALQKSLKDPNNFR 202

RESULT 12
US-09-074-044A-17
Sequence 17, Application US/09074044A
Patent No. 6207458
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MISSOURI
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-17

Query Match 29.3%; Score 527; DB 3; Length 221;
Best Local Similarity 100.0%; Pred. No. 5.5e-48;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 156
QY 61 KNHRIIDLKTKIQKQKQSVQAGTSYRNVLAALQKSLKDPNNFR 106

DB 157 KNHRIIDLKTKIQKQKQSVQAGTSYRNVLAALQKSLKDPNNFR 202

RESULT 13
US-09-074-044A-2
Sequence 2, Application US/09074044A
Patent No. 6207458
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MISSOURI
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-2

Query Match 21.3%; Score 383; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.8e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 60
DB 8 MAEIGEDLDKSDVSSLIPLMKDYMGKISKEKSFLLVVELEKLNVAAPDQDLLEKCL 67
QY 61 KNHRIIDLKTKIQKQKQ 77
DB 66 KNHRIIDLKTKIQKQKQ 84

RESULT 14
US-09-382-155-2
Sequence 2, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24

EARLIER APPLICATION NUMBER: 08/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 84
TYPE: PRT
ORGANISM: HUMAN HERPESVIRUS 8
US-09-382-155-2

Query Match 20.5%; Score 369; DB 3; Length 84;
Best Local Similarity 97.4%; Pred. No. 8.9e-32;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MA1GDDLDKSDVSSILFLMKDYMGRGKISKESKESFLDLYVELEKLNVAPODLLEKCL 60
8 MA1GDDLDKSDVSSILFLMKDYMGRGKISKESKESFLDLYVELEKLNVAPODLLEKCL 67

Qy 61 KNHRIDLKTKIKQYKQ 77
68 KNHRIDLKTKIKQYKQ 84

RESULT 15
US-08-983-502-7
Sequence 7, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yury V. GOLITSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,966
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-7

Query Match 17.4%; Score 313; DB 4; Length 479;
Best Local Similarity 26.8%; Pred. No. 1.4e-24;
Matches 95; Conservative 75; Mismatches 117; Indels 68; Gaps 14;

Qy 3 E1GDDLDKSDVSSILFLMKDYMGRGKISKESKESFLDLYVELEKLNVAPODLLEKCL 62
107 Q1SEVSRSELKSFKFLQOEISKCKLDDDMWLDIFTEMKRVILGEGKIDIKRCAQ 166

Db 63 IHRIDLKTKIKQYKQ-----SVQAGTSYRNVLOA10KSLDPNNFREEPVKSIQ 115
167 INKSLKI-INDYEFESKERSSSLSGSPDFSNGBELGVMTISDP---RE-----Q 215

Qy 116 BSEAFIPQSIPEERIKYMSKPIGICLTIDCIG-----NETEL-----LR 154
216 DES--QTL-DKVVQMSKRGYCLINNENFAKAREKVKLHSIRDRNTHLDAGALT 271

Db 155 DFTSLGYEVCKFLHSMHGISOILGQFACMPHERDYPFCVZVSRGSOVYGVQTH 214
272 TTBEHIFRIKHDCITYEQIYEILKIYQM-DHNMOCFICLISHDKGI1IGTDQOE 330

Qy 215 SGLPLHHRFMWGSFCYLAGKPMFTIQ-----NY---VVSQGLDSSLBYD--GP 264
331 A--PIVELTSCFTGLKCPSLAGKPKVFFIOACQGDNYQKGIPIVETDSSEQYLEMDLSP 388

Qy 265 AMKNVFFKAQKRGKGLCTVHREADFWSLCTADWSLLEQSHSPSLYLOCTSGKLRQ 319
389 QTRVTP-----DEADFLIGMNVNVCVSRNPAGCTWYIGLCSLRE 431

Db

Search completed: September 8, 2004, 05:52:28
Job time : 62 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 ; Search time 58 Seconds
(without alignments)
1695.285 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800
Sequence: 1 MATIGEDLDKSDVSLIFLM.....ITRSDMHFSSVGLTLDVL 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1800	100.0	348	2	AAW69230 I-FLICE-2
2	1800	100.0	348	7	ADA10619 Human inh
3	1774	98.6	366	2	AAW05788 Human MAC
4	1774	98.6	462	3	AAW67419 Usurpin-b
5	1635	90.8	384	2	AAW05791 WRIT alph
6	1635	90.8	480	2	AAW58578 Human CAS
7	1635	90.8	480	2	AAW69715 Human Fin
8	1635	90.8	480	2	AAW69229 I-FLICE-1
9	1635	90.8	480	2	AAW66631 Human CFL
10	1635	90.8	480	2	AAW05787 Human MAC
11	1635	90.8	480	2	AAW57454 Human FLI
12	1635	90.8	480	3	AAW57606 Human apo
13	1635	90.8	480	3	AAW67418 Usurpin-a
14	1635	90.8	480	3	AAW03960 FLICE-11k
15	1635	90.8	480	5	ABW09294 Human FLI
16	1635	90.8	480	7	ADA10615 Human inh
17	1635	90.8	491	3	AAW03964 FLIP with
18	1630	90.6	391	4	AAW09601 Human gen
19	1630	90.6	391	4	AAW01591 Novel hum
20	1630	90.6	391	5	ABW78973 Human apo
21	1630	90.6	391	7	ADCA6232 Human neo
22	1630	90.6	391	7	AAW39801 Human gen
23	1630	90.6	480	2	AAW78903 Human GI
24	1618	89.9	479	2	AAW76625 Human FLI
25	1579	87.7	480	3	AAW59414 Human CIA

26	1554.5	86.4	445	2	AAW90107 Human FLA
27	1554.5	86.4	445	5	AAW26086 Human FLA
28	1228	68.3	302	2	AAW05792 MRIT-ND1
29	1128	62.7	264	2	AAW05790 Human ant
30	1018	56.6	481	2	AAW76632 Mouse CFL
31	1018	56.6	481	3	AAW03958 FLICE-11k
32	1018	56.6	481	5	ABW09295 Mouse FLI
33	1018	56.6	483	2	AAW76626 Murine FLI
34	1006.5	55.9	484	5	ABW09292 Mouse FLI
35	1006.5	55.9	484	6	ABW93983 Amino aci
36	978	54.3	230	2	AAW05793 MRIT-Bam
37	711.5	39.5	291	3	AAW67420 Usurpin-9
38	683	37.9	175	2	AAW05794 MRIT-D/S
39	661.5	36.8	270	5	AAW26110 Human FLA
40	540	30.0	227	2	AAW05795 MRIT beta
41	527	29.3	221	2	AAW78904 Human FLI
42	527	29.3	221	2	AAW76630 Human GI
43	527	29.3	221	2	AAW05789 Human MAC
44	527	29.3	221	2	AAW57455 Human FLI
45	527	29.3	221	3	AAW03959 FLICE-11k

ALIGNMENTS

RESULT 1
AAW69230 standard; protein; 348 AA.
ID
XX
AC AAW69230;
XX
DT 18-FEB-1999 (first entry)
XX
DE I-FLICE-2 protein.
XX
KW I-FLICE-2; FADD like ICB protein; inhibitor; TNFR-1; Alzheimer's disease;
KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
KW viral infection; graft versus host disease; graft rejection.
XX
OS Homo sapiens.
XX
PN WO9831801-AI.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US000969.
XX
PR 21-JAN-1997; 97US-0034205P.
PR 05-AUG-1997; 97US-0054600P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX (UNMI) UNIV MICHIGAN.
XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX
XX WPI: 1998-414100/35.
XX
XX N-PSDB; AAW44807.
XX
XX New inhibitory polypeptides of FLICE - used to develop products for
XX treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
XX autoimmune disorders, viral infection or graft rejection.
XX
XX Claim 9; Fig 4; 118pp; English.
XX
XX This sequence is an inhibitor of of Fas-ligand associated with death
XX domain (FADD) like ICB (I-FLICE) protein, designated I-FLICE-2. The
XX proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
XX the first examples of a naturally occurring catalytically inactive
XX caspase that can act as a dominant negative inhibitor of apoptosis. The
XX polypeptides and agonists can be used for treating e.g. Alzheimer's
XX disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,

CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening

XX Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5,6e-172;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVLEKLNVAPODLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVLEKLNVAPODLLEKCL 60
 QY 61 KNIHRIDLKTKIQKQKQVQAGTSYRNVLOAIOKSLDPNNFREBPVKKSIOSEAF 120
 DB 61 KNIHRIDLKTKIQKQKQVQAGTSYRNVLOAIOKSLDPNNFREBPVKKSIOSEAF 120
 QY 121 LPOSIPERRYKMSKPLGICLIIDCGNETELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSIPERRYKMSKPLGICLIIDCGNETELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 QY 181 QFACMPHRDYDSFVCVLVSRGSSQSVYGVDTHTSGPLHRIIRMFMDSCPYLAGKPKM 240
 DB 181 QFACMPHRDYDSFVCVLVSRGSSQSVYGVDTHTSGPLHRIIRMFMDSCPYLAGKPKM 240
 QY 241 FFIONYVVSQGLLEDSLSLEVDGPMKNVEFKAQKRGCLCTVHREADFMSLCTADMSLE 300
 DB 241 FFIONYVVSQGLLEDSLSLEVDGPMKNVEFKAQKRGCLCTVHREADFMSLCTADMSLE 300
 QY 301 QSHSSPSLYLOCLSQKLRQERGTIPGSGITSEKDMHFSLGICILLDVL 348
 DB 301 QSHSSPSLYLOCLSQKLRQERGTIPGSGITSEKDMHFSLGICILLDVL 348

RESULT 2

ADA10619 standard; protein; 348 AA.

ADA10619;

06-NOV-2003 (first entry)

Human inhibitor of FLICE (I-FLICE-2) protein.

XX Human, I-FLICE-2; inhibitor of FLICE; FADD-like ICE;
 KW tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
 KW CD-95 induced apoptosis; apoptosis associated disease;
 KW Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
 KW ischaemia; septic shock; degenerative liver disease;
 KW cardiovascular disorder; aberrant cell survival; neurologic;
 KW anti-rheumatic; vasotropic; hepatotropic; osteopathic; cardiac;
 KW cerebroprotective; antibacterial; antiarthritis; vasodilator.

OS Homo sapiens.

XX US2003087339-A1.

XX 06-MAY-2003.

XX 21-JAN-1998; 98US-00009893.

XX 21-JAN-1997; 97US-0034205P.

PR 05-AUG-1997; 97US-0054800P.

XX (NIJ/J) NI J.
 XX (ROSE/) ROSEN C. A.
 XX (DIXI/) DIXIT V. M.
 XX (GENT/) GENTZ R. L.
 XX (KENN/) KENNY J. J.

XX NI J., Rosen CA, Dixit VM, Gentz RL, Kenny JJ;

XX WPI; 2003-576674/54.

XX N-PSDB; ADA10618.

PR New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
 PT for treating diseases associated with apoptosis e.g., Alzheimer's
 PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
 PT shock.

XX Claim 1; Fig 4A-4C; 48pp; English.

XX The present invention relates to the isolation of novel human I-FLICE-1
 CC (inhibitor of FLICE (FADD-like ICE)) and I-FLICE-2 proteins, and the
 CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
 CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
 CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
 CC and recombinant methods for producing the I-FLICE proteins. The sequences
 CC e.g. Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
 CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
 CC disorders. They are also useful for diagnosing diseases or disorders
 CC associated with aberrant cell survival in an individual. The present
 CC sequence represents human I-FLICE-2.

XX Sequence 348 AA.

Query Match 100.0%; Score 1800; DB 7; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5,6e-172;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVLEKLNVAPODLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSLIPLMKDYGKGIKSKSFLLVLEKLNVAPODLLEKCL 60
 QY 61 KNIHRIDLKTKIQKQKQVQAGTSYRNVLOAIOKSLDPNNFREBPVKKSIOSEAF 120
 DB 61 KNIHRIDLKTKIQKQKQVQAGTSYRNVLOAIOKSLDPNNFREBPVKKSIOSEAF 120
 QY 121 LPOSIPERRYKMSKPLGICLIIDCGNETELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSIPERRYKMSKPLGICLIIDCGNETELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 QY 181 QFACMPHRDYDSFVCVLVSRGSSQSVYGVDTHTSGPLHRIIRMFMDSCPYLAGKPKM 240
 DB 181 QFACMPHRDYDSFVCVLVSRGSSQSVYGVDTHTSGPLHRIIRMFMDSCPYLAGKPKM 240
 QY 241 FFIONYVVSQGLLEDSLSLEVDGPMKNVEFKAQKRGCLCTVHREADFMSLCTADMSLE 300
 DB 241 FFIONYVVSQGLLEDSLSLEVDGPMKNVEFKAQKRGCLCTVHREADFMSLCTADMSLE 300
 QY 301 QSHSSPSLYLOCLSQKLRQERGTIPGSGITSEKDMHFSLGICILLDVL 348
 DB 301 QSHSSPSLYLOCLSQKLRQERGTIPGSGITSEKDMHFSLGICILLDVL 348

RESULT 3

AA05788 standard; protein; 366 AA.

XX AA05788;

XX 02-AUG-1999 (first entry)

XX Human MACH related inducer of toxicity MCHT alpha 2.

XX MMT alpha 2; MACH related inducer of toxicity; human; apoptosis;
 KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;
 KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
 KW aplastic anaemia; myocardial infarction; therapy.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Active-site 262..266
 XX
 PN MO9318230-A2.
 XX
 PD 15-APR-1999.
 XX
 PF 07-OCT-1998; 98WO-US021132.
 XX
 PR 07-OCT-1997; 97US-00946226.
 XX
 PA (UNIM) UNIV WASHINGTON.
 XX
 PI Chaudhary PM;
 XX
 DR WPI: 1999-277275/23.
 DR N-PSDB; AAX25509.
 XX
 PT Identifying regulators of MACH-related inducer of toxicity.
 XX
 PS Claim 14; Fig 1G; 78pp; English.
 XX
 CC The present sequence represents novel human MACH-related inducer of
 CC toxicity (MMT) isoform MMT alpha 2, a CED-4 homologue. Multiple
 CC isoforms of MMT have been identified, some of which function to induce
 CC caspase dependent apoptosis in mammalian cells, e.g. MMT alpha 1 (see
 CC AAY05787) and MMT beta 1 (see AAY05789), while others have anti-
 CC apoptotic activity, e.g. MMT alpha 2. Selective enhancers and inhibitors
 CC of MMT apoptotic activity can be identified and used to treat diseases
 CC mediated by the dysfunction of programmed cell death or proliferation. A
 CC cell accumulation disorder such as cancer, autoimmune disease, viral
 CC infection, angiogenesis or atherosclerosis is treated by administering an
 CC agent that selectively enhances MMT apoptotic activity, thereby inducing
 CC apoptosis in a subject. A disorder of cell loss, such as a
 CC neurodegenerative disorder, including Alzheimer's disease, Parkinson's
 CC disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
 CC infarction or AIDS can be treated by administering an agent that
 CC selectively inhibits MMT apoptotic activity
 CC
 XX
 SQ Sequence 366 AA;
 Query Match 98.6%; Score 1774; DB 2; Length 366;
 Best Local Similarity 94.5%; Pred. No. 2,5e-169;
 Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDKSDVSSILFLMKDYGKGIKSKSKSFLDLVLEKLNLAAPDQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSILFLMKDYGKGIKSKSKSFLDLVLEKLNLAAPDQDLLEKCL 60
 QY 61 KNHRIIDLTKIKYKQSVGAGTSRVNLAIAIKSLKDPNNR----- 106
 DB 61 KNHRIIDLTKIKYKQSVGAGTSRVNLAIAIKSLKDPNNR----- 106
 QY 107 -----EEPVKKSIOSESAFLPQSIPEERYKSKKPLGICIIIDCIGNETELLADPTSLGY 162
 DB 121 LGAQGEVKKKSIOSESAFLPQSIPEERYKSKKPLGICIIIDCIGNETELLADPTSLGY 180
 QY 163 EVQKFLHLNHHGSIQILGQFACMPERHDVDFYCVAVSGSGSQSYGVQDQTHSGPLHHI 222
 DB 181 EVQKFLHLNHHGSIQILGQFACMPERHDVDFYCVAVSGSGSQSYGVQDQTHSGPLHHI 240
 QY 223 RRMFMGSCCYLAGKPKMFFIQRVYVSDGQLEDSSLLEVDGPKAMKVEPKAKRGGLCTVH 282
 DB 241 RRMFMGSCCYLAGKPKMFFIQRVYVSDGQLEDSSLLEVDGPKAMKVEPKAKRGGLCTVH 300

QY 283 READFFWLSCTADMSLEQSHSSPSLYLQCLISOKLRQERGTIPSGITSKDMHRSLSGC 342
 DB 301 READFFWLSCTADMSLEQSHSSPSLYLQCLISOKLRQERGTIPSGITSKDMHRSLSGC 360
 QY 343 ILIDVL 348
 DB 361 ILIDVL 366
 RESULT 4
 ID AAY67419 standard; protein; 462 AA.
 XX
 AC AAY67419;
 XX
 DT 12-MAY-2000 (first entry)
 XX
 DE Usurpin-beta polypeptide.
 XX
 KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
 KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytosolic; antiParkinsonian; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 PN MO200003023-A1.
 PD 20-JAN-2000.
 XX
 PF 07-JUL-1999; 99WO-CA000615.
 XX
 PR 08-JUL-1998; 98US-0092005P.
 XX
 PA (MERI) MERCK FROSST CANADA INC.
 XX
 PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
 XX
 DR WPI: 2000-160929/14.
 DR N-PSDB; AAZ56988.
 XX
 PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease.
 XX
 PS Claim 6; Fig 10B; 69pp; English.
 XX
 CC The invention provides recombinant nucleic acid molecules encoding
 CC usurpin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
 CC useful for in vitro and in vivo identification of usurpin-procaspase-8
 CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
 CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurpin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurpin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents the
 CC usurpin-beta polypeptide
 CC
 XX
 SQ Sequence 462 AA;
 Query Match 98.6%; Score 1774; DB 3; Length 462;
 Best Local Similarity 94.5%; Pred. No. 3,5e-169;
 Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDKSDVSSILFLMKDYGKGIKSKSKSFLDLVLEKLNLAAPDQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSILFLMKDYGKGIKSKSKSFLDLVLEKLNLAAPDQDLLEKCL 156
 QY 61 KNHRIIDLTKIKYKQSVGAGTSRVNLAIAIKSLKDPNNR----- 106

CC cell, comprising a vector containing FIN-1 encoding DNA, can be used to
 CC produce FIN-1. The vector containing the DNA can be used for producing a
 CC cell which expresses a polypeptide by transforming or transfecting the
 CC cell with it so that the cell expresses the polypeptide encoded the human
 CC cDNA contained in the vector. The polypeptide or its antagonist can be
 CC used in the treatment of patients needing FIN-1 by in-vivo
 CC administration. Conditions which may be treated include viral infection,
 CC tumours (especially solid tumours), ischaemic injury (e.g. stroke or
 CC myocardial infarction), neurodegenerative disorders (e.g. Alzheimer's or
 CC Parkinson's disease), osteoporosis, osteoarthritis, poly cystic kidney
 CC disease, chronic degenerative liver disease, acquired immunodeficiency
 CC syndrome (AIDS) and aplastic anaemia. The polynucleotides may also be
 CC used for chromosome identification

XX Sequence 480 AA:

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 156
 61 KNHRIDLTKTKIOKYKQSVGAGTSYRNVLQALIQSKLDPSNNRRLHNGSKKEQRLKEQ 216
 157 KNHRIDLTKTKIOKYKQSVGAGTSYRNVLQALIQSKLDPSNNRRLHNGSKKEQRLKEQ 216
 107 ----EEPVKKSIOESBAFLPQSIPEERYKMSKPLGICLIIDICIGNETELRLDPTSLGY 162
 217 LGAQOEVPVKKSIOESBAFLPQSIPEERYKMSKPLGICLIIDICIGNETELRLDPTSLGY 276
 163 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCVLVSRGSGQSYGVQDQTHSGPLNHI 222
 277 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCVLVSRGSGQSYGVQDQTHSGPLNHI 336
 223 RRMFMGDSCEPYLAGKPKMFPIQNYVVSDDQLHDSLSLEVDGPMKNVPEFKOKRGLCTVH 282
 337 RRMFMGDSCEPYLAGKPKMFPIQNYVVSDDQLHDSLSLEVDGPMKNVPEFKOKRGLCTVH 396
 283 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
 397 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 7
 AAM69715 standard; protein; 480 AA.

XX AAM69715;

XX 24-NOV-1998 (first entry)

XX Human Casper protein.

XX Casper; caspase-e-ght-related protein; human; apoptosis.

XX Homo sapiens.

XX MO9833883-A1.

XX 06-AUG-1998.

XX 05-FEB-1998; 98MO-US002117.

XX 05-FEB-1997; 97US-00795088.

XX (TULIA-) TULARIK INC.

XX Shu H, Goeddel DV;

XX WPI; 1998-437440/37.

XX N-PSDB; AAV50436.

XX New Casper protein involved in regulation of apoptosis - used, e.g. to
 PT identify specific modulators, identify or isolate similar sequences and
 PT in gene therapy.

XX Claim 1; Page 22-23; 29pp; English.

CC This is the amino acid sequence of a novel human protein, designated
 CC Casper (for caspase-eight-related protein), that is involved in
 CC regulation of apoptosis. The sequence is deduced from an isolated cDNA
 CC clone (see AAV50436). Casper protein interacts with FADD and is recruited
 CC to Fas. It also interacts with caspase-8 and caspase-3, and with TRAF1
 CC and TRAF2. A claimed isolated polypeptide comprises the full-length
 CC Casper amino acid sequence, or a fragment of at least 6 consecutive amino
 CC acid residues including at least one of residues 1-96, 1-202, 1-435, 78-
 CC 480, 192-480, 390-480 or residue 360. The isolated protein, or cells that
 CC express the protein, can be used to screen for agents, e.g. antibodies or
 CC T-cell receptors, that specifically modify the binding of Casper to a
 CC target, and thus its function

XX Sequence 480 AA:

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKESFLDLVLEKLNVAAPQDLLEKCL 156
 61 KNHRIDLTKTKIOKYKQSVGAGTSYRNVLQALIQSKLDPSNNRRLHNGSKKEQRLKEQ 216
 157 KNHRIDLTKTKIOKYKQSVGAGTSYRNVLQALIQSKLDPSNNRRLHNGSKKEQRLKEQ 216
 107 ----EEPVKKSIOESBAFLPQSIPEERYKMSKPLGICLIIDICIGNETELRLDPTSLGY 162
 217 LGAQOEVPVKKSIOESBAFLPQSIPEERYKMSKPLGICLIIDICIGNETELRLDPTSLGY 276
 163 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCVLVSRGSGQSYGVQDQTHSGPLNHI 222
 277 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCVLVSRGSGQSYGVQDQTHSGPLNHI 336
 223 RRMFMGDSCEPYLAGKPKMFPIQNYVVSDDQLHDSLSLEVDGPMKNVPEFKOKRGLCTVH 282
 337 RRMFMGDSCEPYLAGKPKMFPIQNYVVSDDQLHDSLSLEVDGPMKNVPEFKOKRGLCTVH 396
 283 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
 397 READPFMSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 8
 AAM69229 standard; protein; 480 AA.

XX AAM69229;

XX 16-OCT-1998 (first entry)

XX I-FLICE-1 protein.

XX I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
 KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
 KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
 KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
 KW viral infection; graft versus host disease; graft rejection.

XX Homo sapiens.

XX MO9831801-A1.

XX 23-JUL-1998.

PF 21-JAN-1998; 98WO-US000969.
 XX
 PR 21-JAN-1997; 97US-0034205P.
 PR 05-AUG-1997; 97US-0054800P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Ni J, Rosen CA, Dixit VV, Gentz RL, Kenny JJ;
 XX WPI; 1998-414100/35.
 DR N-PSDB; AAV44806.
 XX
 PT New inhibitory polypeptides of FLICE - used to develop products for
 PT treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
 PT autoimmune disorders, viral infection or graft rejection.
 XX
 PS Claim 9; Fig 1; 118pp; English.

CC This sequence is an inhibitor of of Fas-ligand associated with death
 CC domain (PADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The
 CC proteins can inhibit both TNF-1 and CD-95 induced apoptosis. These are
 CC the first examples of a naturally occurring catalytically inactive
 CC caspase that can act as a dominant negative inhibitor of apoptosis. The
 CC polypeptides and agonists can be used for treating e.g. Alzheimer's
 CC disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,
 CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumors, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening
 CC
 XX
 SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 156
 QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
 DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216
 QY 107 -----EPPVKSIQSESAFLPQSIPEERYMKSKPIGICLIIDICIGNETELRLDTFTSLGY 162
 DB 217 LGAQGEFVKKSIQSESAFLPQSIPEERYMKSKPIGICLIIDICIGNETELRLDTFTSLGY 276
 QY 163 EVQKFLHLSMGIISQILGQFACMPBHRDYSFVCVLVSRGSGQSYGVQDTHSGPLPHI 222
 DB 277 EVQKFLHLSMGIISQILGQFACMPBHRDYSFVCVLVSRGSGQSYGVQDTHSGPLPHI 336
 QY 223 RRMFMGDSCPYLAGKPKMFIIQNYVVSQGLDSSLLLEVDPGPMKNGVEFFKQKGLCTVH 282
 DB 337 RRMFMGDSCPYLAGKPKMFIIQNYVVSQGLDSSLLLEVDPGPMKNGVEFFKQKGLCTVH 396
 QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
 DB 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 9
 AAW76631

ID AAW76631 standard; protein; 480 AA.

XX AAW76631;

XX 12-JUL-1999 (first entry)

XX Human CFLIP-L protein.

XX Death effector domain; human; murine; anti-apoptotic; treatment;

KW HIV infection; autoimmune disease; FLIP protein.

XX Homo sapiens.

XX DB19713393-A1.

XX 08-OCT-1998.

PF 01-APR-1997; 97DE-01013393.

PR 01-APR-1997; 97DE-01013393.

XX (TSCN/) TSCNPP J.

XX Tschopp J, Thome M, Burns K, Irmeler M, Hahne M, Schroeder M;
 PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;
 XX WPI; 1998-532710/46.

DR N-PSDB; AAV61937.

XX New DNA encoding for anti-apoptotic gene product - used to treat HIV

PT infections and autoimmune diseases.

XX Claim 20; Fig 4B; 45pp; German.

CC This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases
 CC
 XX
 SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSLIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 156
 QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
 DB 157 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216
 QY 107 -----EPPVKSIQSESAFLPQSIPEERYMKSKPIGICLIIDICIGNETELRLDTFTSLGY 162
 DB 217 LGAQGEFVKKSIQSESAFLPQSIPEERYMKSKPIGICLIIDICIGNETELRLDTFTSLGY 276
 QY 163 EVQKFLHLSMGIISQILGQFACMPBHRDYSFVCVLVSRGSGQSYGVQDTHSGPLPHI 222
 DB 277 EVQKFLHLSMGIISQILGQFACMPBHRDYSFVCVLVSRGSGQSYGVQDTHSGPLPHI 336
 QY 223 RRMFMGDSCPYLAGKPKMFIIQNYVVSQGLDSSLLLEVDPGPMKNGVEFFKQKGLCTVH 282
 DB 337 RRMFMGDSCPYLAGKPKMFIIQNYVVSQGLDSSLLLEVDPGPMKNGVEFFKQKGLCTVH 396
 QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
 DB 397 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 10
 AAY05787
 ID AAY05787 standard; protein; 480 AA.

XX	AAV05787;
XX	02-AUG-1999 (first entry)
DT	Human MACH related inducer of toxicity MRIT alpha 1.
DE	MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis; pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis; KM atherosclerosis; neurodegenerative disease; Alzheimer's disease; KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; KM aplastic anaemia; myocardial infarction; therapy. XX OS Homo sapiens. XX XX Key Location/Qualifiers FH Region 1..165 FT Region /note="death effector domain homology region" FT Region 140..178 FT Region /note="Bcl-2 homology region" FT Region 196..228 FT Region /note="Bcl-2 homology region" FT Region 258..289 FT Region /note="Bcl-2 homology region" FT Region 299..350 FT Region /note="Bcl-2 homology region" FT Region 301..480 FT Region /note="caspase homology region" FT Region 356..397 FT FT /note="Bcl-2 homology region" PT Active-site 358..362 PN MO9918230-A2. XX XX 15-APR-1999. XX XX PF 07-OCT-1998; 98WO-US021132. XX PR 07-OCT-1997; 97US-00946226. XX XX PA (UNIW) UNIV WASHINGTON. XX XX Chaudhary PM; DR MPI; 1999-277275/23. DR N-PDB; AAX35508. XX PT Identifying regulators of MACH-related inducer of toxicity. PS Example 1; Fig 1F; 78pp; English. XX XX The present sequence represents novel human MACH-related inducer of CC toxicity (MRIT) isoform MRIT alpha 1, a CED-4 homologe that interacts CC simultaneously with caspases and Bcl-2 family polypeptides, and which has CC pro-apoptotic activity. Multiple isoforms of MRIT have been identified, CC some of which function to induce caspase dependent apoptosis in mammalian CC cells, e.g. MRIT alpha 1 and MRIT beta 1 (see AA05789), while others CC have anti-apoptotic activity, e.g. MRIT alpha 2 (see AA05788). MRIT CC alpha 1 includes an N-terminal death effector domain and a C-terminal CC caspase homology domain, but is not a cysteine protease. Selective CC enhancers and inhibitors of MRIT apoptotic activity can be identified and CC used to treat diseases mediated by the dysfunction of programmed cell CC death or proliferation. A cell accumulation disorder such as cancer, CC autoimmune disease, viral infection, angiodysplasia or atherosclerosis is CC treated by administering an agent that selectively enhances MRIT CC apoptotic activity, thereby inducing apoptosis in a subject. A disorder CC of cell loss, such as a neurodegenerative disorder, including Alzheimer's CC disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic CC anemia, myocardial infarction or AIDS can be treated by administering an CC agent that selectively inhibits MRIT apoptotic activity XX XX Sequence 480 AA; XQ

Query Match:	90.8%	Score 1635;	DB 2;	Length 480;
Best Local Similarity	94.1%	Pred. No. 3.6e-155;		
Matches 319;	Conservative	2;	Mismatches	0;
			Indels	18;
			Gaps	1

QY	1	MAEIGEDLDKSDVSSLI	FLMDYDYGKGISKEKSF	LDLVELEKXNLVAPDQDL	EKCL	60
DB	97	MAEIGEDLDKSDVSSLI	FLMDYDYGKGISKEKSF	LDLVELEKXNLVAPDQDL	EKCL	156
QY	61	KNIHRIIDLTKIK	QTKKQSVQAGTSYRNV	LOAALQKSLKPNPNFR	-----	106
DB	157	KNIHRIIDLTKIK	QTKKQSVQAGTSYRNV	LOAALQKSLKPNPNFR	-----	106
QY	107	---EEPVKKSIQESEA	FLPOSIPERKMKSKPLGICLI	IIDICGNTELLRDTFTSLG	Y	162
DB	217	LGAGQCPVPKKSQ	GESEAFLPQSIPEERKMKSKPLGICLI	IIDICGNTELLRDTFTSLG	Y	276
QY	163	EVQKFLHLSMHGISQ	ILIQFACMPBEHRDYSFVCV	LVSRGSGSVGVGDTHSGPLPHI		222
DB	277	EVQKFLHLSMHGISQ	ILIQFACMPBEHRDYSFVCV	LVSRGSGSVGVGDTHSGPLPHI		336
QY	223	RNFEMGDSCEPYLAG	KPKMFIONVYVSDGLEDS	SLLEVGPAMKRVFPAQRKGLCTVH		282
DB	337	RNFEMGDSCEPYLAG	KPKMFIONVYVSDGLEDS	SLLEVGPAMKRVFPAQRKGLCTVH		396
QY	283	READPFWSLCTADM	SLLEQSHSSPSLYIQCL	SQKLRQER		321
DB	397	READPFWSLCTADM	SLLEQSHSSPSLYIQCL	SQKLRQER		435

RESULT 11		
ID	AAV57454	standard; protein; 480 AA.
XX	AAV57454	
AC	AAV57454;	
XX		
DT	25-FEB-2000	(first entry)
DE		
XX		
DE		Human FLICE-like inhibitory protein long form protein sequence.
XX		
KM		Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
KW		FLICE-like inhibitory protein short form; apoptosis inhibitor;
KW		arteriosclerosis; vascular wall inflammation; vascular injury;
KW		Fas ligand-mediated apoptosis; arteriosclerosis; transplant.
XX		
OS		Homo sapiens.
XX		
XX		
PN	WO942570-A1.	
XX		
PD	26-AUG-1993.	
XX		
PF	19-FEB-1993;	99WO-US003558.
XX		
PR	20-FEB-1998;	98US-0075471P.
XX		
PA	(SELI-) ST ELIZABETH'S MEDICAL CENT	BOSTON INC.
XX		
PI	Walsh K;	
XX		
DR	WPI; 1999-527469/44.	
XX		
DR	N-PDB; AAZ39040.	
XX		
PT		Treating conditions characterized by vascular wall inflammation.
XX		
PS	Claim 5; Page 69-71; 105pp;	English.
XX		

CC	The present sequence represents human FLICE-like inhibitory protein long
CC	form, designated FLIP-L. The present invention describes a new treatment
CC	of a condition characterized by vascular wall inflammation in a subject
CC	comprising administering a FLIP molecule to inhibit Fas ligand-mediated
CC	apoptosis of vascular endothelial cells in the subject. The method can be
CC	used to treat arteriosclerosis, transplant arteriosclerosis and vascular
CC	injury
CC	

SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3,6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 156

DB 61 KNHRIIDLKTKIOKTKOSVQAGTSYRNVLCQAIOKSLKDPSPNNFR----- 106
 157 KNHRIIDLKTKIOKTKOSVQAGTSYRNVLCQAIOKSLKDPSPNNFRHNGRSKEQRLKEQ 216

QY 107 ----EEPVKKSIOESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 162
 217 LGAQGEFVKKSIOESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 276

DB 163 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTHTSGPLPHHI 222
 277 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTHTSGPLPHHI 336

QY 223 RRMFMGDSCEPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNGVEFKAQKRGCLTVH 282
 337 RRMFMGDSCEPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNGVEFKAQKRGCLTVH 396

DB 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

QY DB

RESULT 12
 AAY57606
 ID AAY57606 standard; protein; 480 AA.
 XX
 AC AAY57606;
 DT 10-MAR-2000 (first entry)
 XX
 DE Human apoptosis associated protein HAPOP-1.
 XX
 KW Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
 KW antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator;
 KW cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer;
 KW immune disorder; rheumatoid arthritis; systemic lupus erythematosus;
 KW reproductive disorder; tumour; gastrointestinal disorder; cirrhosis;
 KW colitis; hepatitis; pancreatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO9958662-A2.
 PD 18-NOV-1999.
 XX
 PF 11-MAY-1999; 99WO-US010386.
 XX
 PR 13-MAY-1998; 98US-00078402.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Corley NC, Guegler KU, Patterson C, Baughn M;
 DR WPI: 2000-062303/05.
 XX
 DR N-PSDB; AAZ47926.
 XX
 PT New protein for diagnosing, treating or preventing disorders associated
 PT with increased or decreased apoptosis.
 XX
 PS Claim 1; Page 70-71; 81pp; English.
 CC The present sequence represents a human apoptosis associated protein
 CC designated HAPOP-1. HAPOP proteins are apoptosis regulators which have
 CC antiarteriosclerotic, cytostatic, antiarthritic and hepatotropic

CC activity. A pharmaceutical composition comprising HAPOP in conjunction
 CC with a carrier, a purified antagonist of HAPOP, vectors and agonists of
 CC HAPOP, are administered for diagnosing, treating or preventing disorders
 CC associated with increased or decreased apoptosis, e.g. cell proliferative
 CC disorders such as atherosclerosis, arteriosclerosis and cancers; immune
 CC disorders such as rheumatoid arthritis, systemic lupus erythematosus;
 CC reproductive disorders such as prostate cancer, endometrial and ovarian
 CC tumours; and gastrointestinal disorders such as cirrhosis, colitis,
 CC hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins
 CC may be useful to detect and quantitate expression of HAPOP genes which
 CC are correlated with diseases and are also useful to detect differences in
 CC the chromosomal location due to translocation, inversion etc., among
 CC normal, carrier, or affected individuals. The combination of the
 CC therapeutic agents may act synergistically to effect the treatment or
 CC prevention of various disorders providing improved efficacy with lower
 CC dosages of each agent and thus reducing the potential for adverse side
 CC effects

SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 3; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3,6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 60
 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVLEKLNVAAPQDLLEKCL 156

DB 61 KNHRIIDLKTKIOKTKOSVQAGTSYRNVLCQAIOKSLKDPSPNNFR----- 106
 157 KNHRIIDLKTKIOKTKOSVQAGTSYRNVLCQAIOKSLKDPSPNNFRHNGRSKEQRLKEQ 216

QY 107 ----EEPVKKSIOESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 162
 217 LGAQGEFVKKSIOESAEFLPOSIPPEERYKMKSKPLGCLIIDICGNTELLRDTFTSLGY 276

DB 163 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTHTSGPLPHHI 222
 277 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSGSVYGVDTHTSGPLPHHI 336

QY 223 RRMFMGDSCEPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNGVEFKAQKRGCLTVH 282
 337 RRMFMGDSCEPYLAGKPKKFFIIONVYVSDGLEDSLLEVDGPMKNGVEFKAQKRGCLTVH 396

DB 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

QY DB

RESULT 13
 AAY67418
 ID AAY67418 standard; protein; 480 AA.
 XX
 AC AAY67418;
 DT 12-MAY-2000 (first entry)
 XX
 DE Usurpin-alpha polypeptide.
 XX
 KW Usurpin-alpha; deach effector domain; DED; prodomain; usurpin-beta;
 KW usurpin-gamma; procaspase-8; C95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytostatic; antiparkinsonian; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 PN WO200003023-A1.
 PD 20-JAN-2000.
 XX
 PF 07-JUL-1999; 99WO-CA000615.
 XX
 PR 08-JUL-1998; 98US-0092005P.
 XX

PA (MERI) MERCK FROST CANADA INC.
 XX
 PI Nicholson DM, Rasper DM, Xanthoudakis S, Roy S;
 XX WPI; 2000-160929/14.
 DR N-PSDB; AAZ56987.
 XX
 PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease.
 XX
 XX Claim 6; Fig 9B; 69pp; English.
 XX
 CC The invention provides recombinant nucleic acid molecules encoding
 CC usurin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurin-beta or usurin-gamma. Usurin polypeptides are
 CC useful for in vitro and in vivo identification of usurin-procaspase-8
 CC interaction inhibitor. Usurin is useful as modulator of the sensitivity
 CC of cells to CD95 (Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95 (Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents the
 CC usurin-alpha polypeptide
 XX
 SO Sequence 480 AA:
 XX
 Query Match 90.8%; Score 1635; DB 3; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKESFLDLVVELKNTLVAPQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKISKESFLDLVVELKNTLVAPQDLLEKCL 156
 QY 61 KNIRHIDLTKIKYKQSYVAGAGTSYRNVLAQAIQKSLKDPNNFR----- 106
 DB 157 KNIRHIDLTKIKYKQSYVAGAGTSYRNVLAQAIQKSLKDPNNFRHNGRKEQRLKEQ 216
 QY 107 -----EEPVKKSIQESAEFLPQSIIPERYKKKSPGLGICIIIDICINETELRLDRTTSIGY 162
 DB 217 LGAQGEFVKKSIQESAEFLPQSIIPERYKKKSPGLGICIIIDICINETELRLDRTTSIGY 276
 QY 163 EVQKFLHLSMHGISQILGFPACMPERHDYDFVCVLVSRGSGQSYGVDOQTHSGPLPHI 222
 DB 277 EVQKFLHLSMHGISQILGFPACMPERHDYDFVCVLVSRGSGQSYGVDOQTHSGPLPHI 336
 QY 223 RRMFMGDSCTYLAGKPMFPIQNYVVSQGLEDSLLLEVDPGPMKNVFEKQKRGCLCTVH 282
 DB 337 RRMFMGDSCTYLAGKPMFPIQNYVVSQGLEDSLLLEVDPGPMKNVFEKQKRGCLCTVH 396
 QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
 DB 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435
 RESULT 14
 ID AAB03960 standard; protein; 480 AA.
 XX AAB03960;
 AC
 XX 26-FEB-2001 (first entry)
 DT
 XX
 DE FLICE-1-like inhibitor protein (Genbank Accession No. 2253679).
 XX
 CC Chimeric protein; fusion protein; FLICE 1-like inhibitor protein; FLIP;
 CC Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
 CC tumour specific antigen; immune response; therapy; prophylaxis;
 CC diagnosis; HIV; human immunodeficiency syndrome; AIDS;

KY acquired immune deficiency syndrome; human.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 PN W0200059935-A1.
 XX
 PD 12-OCT-2000.
 XX
 XX 05-APR-2000; 2000MO-US009002.
 PF
 XX 05-APR-1999; 99US-0127867P.
 PR
 XX 06-APR-1999; 99US-0128021P.
 XX
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 PA (PAPA/) PAPA C.
 PA (ALGE/) ALGECIRAS-SCHMINICH A.
 PI PAPA C, Algeciras-Schminich A;
 XX
 DR WPI; 2000-664988/64.
 XX
 PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
 PT comprises portion of anti-apoptotic polypeptide linked to a transport
 PT group.
 XX
 PS Disclosure; Page 79-81; 89pp; English.
 XX
 CC A chimeric group or fusion peptide which comprises a portion of an anti-
 CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in
 CC combination with a transport group is described. The transport group is
 CC capable of transporting the chimeric group or fusion peptide across the
 CC cell membrane. The anti-apoptotic polypeptide is FLICE-1-like inhibitor
 CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by
 CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus
 CC shutting off the downstream Fas signaling pathway. The chimeric group
 CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by
 CC bringing them into contact with T cells. The chimeric group is useful for
 CC expanding T cells in vitro e.g. T cells specific for particular antigens
 CC such as tumour-specific antigen, for enhancing immune response and to
 CC inhibit the apoptosis of chronically activated T cells e.g. activated
 CC CD4⁺ T cells in HIV infected patients. The chimeric group is also useful
 CC for therapeutic, prophylactic or diagnosis of intracellular delivery of
 CC small molecules and macromolecules such as anti-apoptotic polypeptides
 CC and nucleic acids encoding such polypeptides
 XX
 SO Sequence 480 AA:
 XX
 Query Match 90.8%; Score 1635; DB 3; Length 480;
 Best Local Similarity 94.1%; Pred. No. 3.6e-155;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
 QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKISKESFLDLVVELKNTLVAPQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKISKESFLDLVVELKNTLVAPQDLLEKCL 156
 QY 61 KNIRHIDLTKIKYKQSYVAGAGTSYRNVLAQAIQKSLKDPNNFR----- 106
 DB 157 KNIRHIDLTKIKYKQSYVAGAGTSYRNVLAQAIQKSLKDPNNFRHNGRKEQRLKEQ 216
 QY 107 -----EEPVKKSIQESAEFLPQSIIPERYKKKSPGLGICIIIDICINETELRLDRTTSIGY 162
 DB 217 LGAQGEFVKKSIQESAEFLPQSIIPERYKKKSPGLGICIIIDICINETELRLDRTTSIGY 276
 QY 163 EVQKFLHLSMHGISQILGFPACMPERHDYDFVCVLVSRGSGQSYGVDOQTHSGPLPHI 222
 DB 277 EVQKFLHLSMHGISQILGFPACMPERHDYDFVCVLVSRGSGQSYGVDOQTHSGPLPHI 336
 QY 223 RRMFMGDSCTYLAGKPMFPIQNYVVSQGLEDSLLLEVDPGPMKNVFEKQKRGCLCTVH 282
 DB 337 RRMFMGDSCTYLAGKPMFPIQNYVVSQGLEDSLLLEVDPGPMKNVFEKQKRGCLCTVH 396
 QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321

DB 397 READFWSLCTADMSLLEQSHSPSLYLQCLSQLRQER 435

RESULT 15

AB09294
ID ABB09294 standard; protein; 480 AA.

XX ABB09294;

XX 15-JUL-2002 (first entry)

DE Human FLIP-c protein SEQ ID NO:11.

XX Human; FLIP-c; caspase 8 dominant negative regulator; anti-inflammatory;

XX anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;

XX phosphorochiolate; antisense modulation; infection; inflammation; tumour.

OS Homo sapiens.

XX WO200224717-A1.

XX 28-MAR-2002.

XX 14-SEP-2001; 2001WO-US028732.

XX 20-SEP-2000; 2000US-00666269.

XX (ISIS-) ISIS PHARM INC.

XX Ackermann EJ, Bennett CF, Zhang H, Watt AT, Rickerts W, Dean NM;

XX WPI; 2002-404948/43.

XX N-PSDB; ABL52333.

XX Novel antisense compound that hybridizes and inhibits nucleic acid

XX encoding a natural dominant negative regulator of caspase 8, FLIP-c,

XX useful for preventing or delaying infection, inflammation or tumor

XX formation.

XX Example 13; Page 118-120; 154pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length

XX targeted to a nucleic acid molecule (II) encoding a natural dominant

XX negative regulator of caspase 8, FLIP-c, where (I) specifically

XX hybridizes with and inhibits expression of the protein, or specifically

XX hybridizes with at least an 8-nucleobase portion of an active site on

XX (II). (I) has anti-inflammatory and anti-tumour activities. (I) is an

XX inhibitor of FLIP-c expression, a modulator of apoptosis and can be used

XX in antisense gene therapy. (I) is useful for inhibiting the expression of

XX FLIP-c in cells or tissues, and for treating an animal having a disease

XX or condition associated with FLIP-c. (I) is also useful for modulating

XX apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or

XX caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is

XX also useful for diagnostics, therapeutics, prophylaxis, as research

XX reagents and kits, for distinguishing functions of various members of a

XX biological pathway, and in antisense gene therapy. (I) is also useful

XX prophylactically, e.g., to prevent or delay infection, inflammation or

XX tumour formation. The present sequence represents human FLIP-c as given

XX in an example from the present invention

XX Sequence 480 AA;

XX

XX

XX

XX

DB 157 KNIRHIDLKTKIQKYKQSVQAGTSYRNVLQAIOKSLKDPNNFRLHNGRSKEQRLKEQ 216

QY 107 -----EEPVKKSIOESFAFLPQSIPEERYKMKSKPIGICLIIDCIGNETELLRDPTSLGY 162

DB 217 LGAQOEPVKKSIOESFAFLPQSIPEERYKMKSKPIGICLIIDCIGNETELLRDPTSLGY 276

QY 163 EVOKFLHLSMHG:SQILGQFACMPEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPLHI 222

DB 277 EVOKFLHLSMHG:SQILGQFACMPEHRDYSFVCVLVSRGSGSVYGVQDTHSGLPLHI 336

QY 223 RRMFMGDSCTYLAGKPMFFIQYVVSQQLDSSLLLEVDPAMKVEFKQKGLCTVH 282

DB 337 RRMFMGDSCTYLAGKPMFFIQYVVSQQLDSSLLLEVDPAMKVEFKQKGLCTVH 396

QY 283 READFWSLCTADMSLLEQSHSPSLYLQCLSQLRQER 321

DB 397 READFWSLCTADMSLLEQSHSPSLYLQCLSQLRQER 435

Search completed: September 8, 2004, 05:50:06

Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:50:49 ; Search time 1037 Seconds
(without alignments)
105.731 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAFIGDLDKSPVSSLIPLM.....ITSDKMFSLGCLLDVL 348

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues
Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubpaa/US10C_NEW_PUB.pep:*
17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1800	100.0	348	10 US-09-009-893-6	Sequence 6, Appl1
2	1800	100.0	348	16 US-10-713-208-6	Sequence 6, Appl1
3	1635	90.8	480	9 US-09-861-270-2	Sequence 2, Appl1
4	1635	90.8	480	9 US-09-410-194-11	Sequence 11, Appl1
5	1635	90.8	480	9 US-09-410-194-17	Sequence 17, Appl1
6	1635	90.8	480	10 US-09-009-893-2	Sequence 2, Appl1
7	1635	90.8	480	10 US-09-471-749-1	Sequence 1, Appl1
8	1635	90.8	480	16 US-10-713-208-2	Sequence 2, Appl1
9	1630	90.6	391	10 US-09-764-861-37	Sequence 37, Appl1
10	1630	90.6	391	12 US-09-764-861-37	Sequence 37, Appl1
11	1630	90.6	391	14 US-10-103-313-318	Sequence 318, App
12	1630	90.6	391	14 US-10-115-928-37	Sequence 37, Appl1
13	1579	87.7	480	16 US-10-408-765A-275	Sequence 275, App
14	1554.5	86.4	445	12 US-09-935-223-2	Sequence 2, Appl1
15	1018	56.6	481	9 US-09-410-194-12	Sequence 12, Appl1

16	1018	56.6	481	9 US-09-410-194-19	Sequence 19, Appl1
17	1006.5	55.9	484	13 US-10-005-821-2	Sequence 2, Appl1
18	527	29.3	221	9 US-09-410-194-15	Sequence 15, Appl1
19	527	29.3	221	9 US-09-410-194-22	Sequence 22, Appl1
20	391	21.7	76	9 US-09-864-761-35073	Sequence 35073, A
21	313	17.4	479	9 US-09-410-194-20	Sequence 20, Appl1
22	313	17.4	479	10 US-09-851-873-101	Sequence 101, App
23	313	17.4	479	15 US-10-368-438-7	Sequence 7, Appl1
24	311.5	17.3	478	10 US-09-009-893-3	Sequence 3, Appl1
25	311.5	17.3	478	16 US-10-713-208-3	Sequence 3, Appl1
26	304.5	16.9	464	15 US-10-368-438-18	Sequence 18, Appl1
27	304.5	16.9	496	12 US-10-232-884-6	Sequence 6, Appl1
28	302.5	16.8	496	9 US-09-952-768-4	Sequence 4, Appl1
29	302.5	16.8	496	12 US-10-668-955-4	Sequence 4, Appl1
30	296.5	16.5	476	9 US-09-954-697-27	Sequence 27, Appl1
31	277	15.4	56	16 US-10-627-571-5	Sequence 5, Appl1
32	277	15.4	56	16 US-10-627-571-7	Sequence 7, Appl1
33	261.5	14.5	335	15 US-10-368-438-16	Sequence 16, Appl1
34	248.5	13.8	521	9 US-09-962-834A-2	Sequence 2, Appl1
35	248.5	13.8	521	10 US-09-851-873-103	Sequence 103, App
36	248.5	13.8	521	14 US-10-439-576-2	Sequence 2, Appl1
37	248.5	13.8	571	9 US-09-410-194-21	Sequence 21, Appl1
38	244	13.6	479	9 US-09-952-768-2	Sequence 2, Appl1
39	244	13.6	479	9 US-09-954-697-33	Sequence 33, Appl1
40	244	13.6	479	10 US-09-009-893-4	Sequence 4, Appl1
41	244	13.6	479	12 US-10-668-955-2	Sequence 2, Appl1
42	244	13.6	479	16 US-10-713-208-4	Sequence 4, Appl1
43	237	13.2	56	16 US-10-627-571-6	Sequence 6, Appl1
44	228	12.7	286	9 US-09-862-915-1	Sequence 1, Appl1
45	227.5	12.6	389	14 US-10-280-670-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-009-893-6
Sequence 6, Application US/09009893
Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA N.
APPLICANT: GENTZ, REINER J.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
TITLE OF INVENTION: NEGROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0970002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 348 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-009-893-6

Query Match 100.0%; Score 1800; DB 10; Length 348;
 Best Local Similarity 100.0%; Pred. No. 3.1e-170;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKNTLVAPDQDLLEKCL 60
 DB 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKNTLVAPDQDLLEKCL 60
 QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFREEPVKKSIOESBAF 120
 DB 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFREEPVKKSIOESBAF 120
 QY 121 LPOSTPEERYKMKSKPLGICLIIDICGNTELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSTPEERYKMKSKPLGICLIIDICGNTELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 QY 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTQTHSGPLPHIRRMFGDSCPYLAGKPKM 240
 DB 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTQTHSGPLPHIRRMFGDSCPYLAGKPKM 240
 QY 241 FFIQNYVSDGQLEDSLSLEVDPAMKQVEFKAQKRGKCTVHREADFWSLCTADMSLLE 300
 DB 241 FFIQNYVSDGQLEDSLSLEVDPAMKQVEFKAQKRGKCTVHREADFWSLCTADMSLLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERGTFPGSGITTEKDMHFSSLGCTLLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERGTFPGSGITTEKDMHFSSLGCTLLDVL 348

RESULT 2
 US-10-713-208-6
 Sequence 6, Application US/10713208
 Publication No. US20040121387A1
 GENERAL INFORMATION:
 APPLICANT: NI et al.
 TITLE OF INVENTION: 1-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 at
 FILE REFERENCE: PF381C1D1
 CURRENT APPLICATION NUMBER: US/10/713,208
 PRIOR FILING DATE: 2003-11-17
 PRIOR APPLICATION NUMBER: US 09/489,155
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US 09/009,893
 PRIOR FILING DATE: 1998-01-21
 PRIOR APPLICATION NUMBER: US 60/054,800
 PRIOR FILING DATE: 1997-08-05
 PRIOR APPLICATION NUMBER: US 60/034,205
 PRIOR FILING DATE: 1997-01-21
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 6
 LENGTH: 348
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-713-208-6

Query Match 100.0%; Score 1800; DB 16; Length 348;
 Best Local Similarity 100.0%; Pred. No. 3.1e-170;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKNTLVAPDQDLLEKCL 60

DB 1 MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKNTLVAPDQDLLEKCL 60
 QY 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFREEPVKKSIOESBAF 120
 DB 61 KNHRIIDLKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFREEPVKKSIOESBAF 120
 QY 121 LPOSTPEERYKMKSKPLGICLIIDICGNTELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 DB 121 LPOSTPEERYKMKSKPLGICLIIDICGNTELLRDTFTSLGYEVQKFLHSMHGISOILG 180
 QY 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTQTHSGPLPHIRRMFGDSCPYLAGKPKM 240
 DB 181 QPACMEHRDYSFVCVLVSRGSGSVYGVDTQTHSGPLPHIRRMFGDSCPYLAGKPKM 240
 QY 241 FFIQNYVSDGQLEDSLSLEVDPAMKQVEFKAQKRGKCTVHREADFWSLCTADMSLLE 300
 DB 241 FFIQNYVSDGQLEDSLSLEVDPAMKQVEFKAQKRGKCTVHREADFWSLCTADMSLLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERGTFPGSGITTEKDMHFSSLGCTLLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERGTFPGSGITTEKDMHFSSLGCTLLDVL 348

RESULT 3
 US-09-861-270-2
 Sequence 2, Application US/09861270
 Patent No. US20020052474A1
 GENERAL INFORMATION:
 APPLICANT: Su, Hong-Bing
 TITLE OF INVENTION: Regulators of Apoptosis
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Science & Technology Law Group
 STREET: 75 Denise Drive
 CITY: Hillsborough
 STATE: California
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/861,270
 FILING DATE: 18-May-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/795,088
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman, Richard A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 480 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-861-270-2

Query Match 90.8%; Score 1635; DB 9; Length 480;
 Best Local Similarity 94.1%; Pred. No. 1.3e-153;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;


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QY      1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLELEKLNVAPODLLEKCL 60
DB      97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLELEKLNVAPODLLEKCL 156
QY      61 KNHRIDLTXTKIQKXKOSVQAGTSYRNVLOAIOKSLKDPNNFR----- 106
DB      157 KNHRIDLTXTKIQKXKOSVQAGTSYRNVLOAIOKSLKDPNNFRNLNGSKEQRLKEQ 216
QY      107 ---EEPVKKSIOESBAFLPQSIPEERYKMKSPGLGICLIIDICIGNETELLRDFTFTSLGY 162
DB      217 LGAQOEPPVKKSIOESBAFLPQSIPEERYKMKSPGLGICLIIDICIGNETELLRDFTFTSLGY 276
QY      163 EVOKFHLHSMHGISOILQGFACMPBHRDYDSFVCVLYSRGGSQSYGVDTQHSGLPLHHI 222
DB      277 EVOKFHLHSMHGISOILQGFACMPBHRDYDSFVCVLYSRGGSQSYGVDTQHSGLPLHHI 336
QY      223 RRMFMGDSCPYLAGKPKMFFIONVYVSDGQLEDSLSLEVDPAMKNVEFFKQKSGLCTVH 282
DB      337 RRMFMGDSCPYLAGKPKMFFIONVYVSDGQLEDSLSLEVDPAMKNVEFFKQKSGLCTVH 396
QY      283 READFFWMSLCTADMSLLEQSHSSPSLYIQCLSQKLRQER 321
DB      397 READFFWMSLCTADMSLLEQSHSSPSLYIQCLSQKLRQER 435

RESULT 4
US-09-410-194-11
; Sequence 11, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imtler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-11

Query Match      90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 1,3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY      1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLELEKLNVAPODLLEKCL 60
DB      97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLELEKLNVAPODLLEKCL 156
QY      61 KNHRIDLTXTKIQKXKOSVQAGTSYRNVLOAIOKSLKDPNNFR----- 106
DB      157 KNHRIDLTXTKIQKXKOSVQAGTSYRNVLOAIOKSLKDPNNFRNLNGSKEQRLKEQ 216
QY      107 ---EEPVKKSIOESBAFLPQSIPEERYKMKSPGLGICLIIDICIGNETELLRDFTFTSLGY 162
DB      217 LGAQOEPPVKKSIOESBAFLPQSIPEERYKMKSPGLGICLIIDICIGNETELLRDFTFTSLGY 276

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QY      163 EVOKFHLHSMHGISOILQGFACMPBHRDYDSFVCVLYSRGGSQSYGVDTQHSGLPLHHI 222
DB      277 EVOKFHLHSMHGISOILQGFACMPBHRDYDSFVCVLYSRGGSQSYGVDTQHSGLPLHHI 336
QY      223 RRMFMGDSCPYLAGKPKMFFIONVYVSDGQLEDSLSLEVDPAMKNVEFFKQKSGLCTVH 282
DB      337 RRMFMGDSCPYLAGKPKMFFIONVYVSDGQLEDSLSLEVDPAMKNVEFFKQKSGLCTVH 396
QY      283 READFFWMSLCTADMSLLEQSHSSPSLYIQCLSQKLRQER 321
DB      397 READFFWMSLCTADMSLLEQSHSSPSLYIQCLSQKLRQER 435

RESULT 5
US-09-410-194-17
; Sequence 17, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imtler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-17

Query Match      90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 1,3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY      1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLELEKLNVAPODLLEKCL 60
DB      97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVLELEKLNVAPODLLEKCL 156
QY      61 KNHRIDLTXTKIQKXKOSVQAGTSYRNVLOAIOKSLKDPNNFR----- 106
DB      157 KNHRIDLTXTKIQKXKOSVQAGTSYRNVLOAIOKSLKDPNNFRNLNGSKEQRLKEQ 216
QY      107 ---EEPVKKSIOESBAFLPQSIPEERYKMKSPGLGICLIIDICIGNETELLRDFTFTSLGY 162
DB      217 LGAQOEPPVKKSIOESBAFLPQSIPEERYKMKSPGLGICLIIDICIGNETELLRDFTFTSLGY 276
QY      163 EVOKFHLHSMHGISOILQGFACMPBHRDYDSFVCVLYSRGGSQSYGVDTQHSGLPLHHI 222
DB      277 EVOKFHLHSMHGISOILQGFACMPBHRDYDSFVCVLYSRGGSQSYGVDTQHSGLPLHHI 336
QY      223 RRMFMGDSCPYLAGKPKMFFIONVYVSDGQLEDSLSLEVDPAMKNVEFFKQKSGLCTVH 282
DB      337 RRMFMGDSCPYLAGKPKMFFIONVYVSDGQLEDSLSLEVDPAMKNVEFFKQKSGLCTVH 396
QY      283 READFFWMSLCTADMSLLEQSHSSPSLYIQCLSQKLRQER 321

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Db 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 6

US-09-009-893-2
; Sequence 2, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NT, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENIZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HERSMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-893-2

Query Match 90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKGISKEKSFLDLVELEKTLNVAPOQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKGISKEKSFLDLVELEKTLNVAPOQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQKTKQSVQAGTSYRNVLAALQKSLKDPNNFR----- 106
DB 157 KNHRIIDLTKTKIQKTKQSVQAGTSYRNVLAALQKSLKDPNNFRFLHNGRSKEQRLKEQ 216
QY 107 ----EEPVKKSIOSESEAFLOPSIPERRYKMKSKPAGICLIDICIGNETELLADTFTSLGY 162
DB 217 LGAQOEVPKKSIOSESEAFLOPSIPERRYKMKSKPAGICLIDICIGNETELLADTFTSLGY 276
QY 163 EVQKFLHLSMHGSIQILGQFACMPERHDYDSFCVLSVRGSGSQSVYGVVDQTHSGPLNHI 222
DB 277 EVQKFLHLSMHGSIQILGQFACMPERHDYDSFCVLSVRGSGSQSVYGVVDQTHSGPLNHI 336

QY 223 RRMFMGDSCTPYLAGKPMFFIQQNVYVSDQLEDSSLEVDGPAMKNVEFFKQKGLCTVH 282

DB 337 RRMFMGDSCTPYLAGKPMFFIQQNVYVSDQLEDSSLEVDGPAMKNVEFFKQKGLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321

DB 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 7

US-09-471-749-1
; Sequence 1, Application US/09471749
; Publication No. US20030124113A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/471,749
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/078,402
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0519 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TRP1PLB02
; CLONE: 157658
US-09-471-749-1

Query Match 90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.3e-153;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGKGISKEKSFLDLVELEKTLNVAPOQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGKGISKEKSFLDLVELEKTLNVAPOQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQKTKQSVQAGTSYRNVLAALQKSLKDPNNFR----- 106
DB 157 KNHRIIDLTKTKIQKTKQSVQAGTSYRNVLAALQKSLKDPNNFRFLHNGRSKEQRLKEQ 216
QY 107 ----EEPVKKSIOSESEAFLOPSIPERRYKMKSKPAGICLIDICIGNETELLADTFTSLGY 162
DB 217 LGAQOEVPKKSIOSESEAFLOPSIPERRYKMKSKPAGICLIDICIGNETELLADTFTSLGY 276

CURRENT APPLICATION NUMBER: US/10/408,765A
 CURRENT FILING DATE: 2003-04-04
 NUMBER OF SEQ ID NOS: 3077
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 275
 LENGTH: 480
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-10-408-765A-275

Query Match 87.7%; Score 1579; DB 16; Length 480;
 Best Local Similarity 91.2%; Pred. No. 5,1e-148;
 Matches 309; Conservative 4; Mismatches 8; Indels 18; Gaps 1;

QY 1 MAIGEDLDKSDVSLIFLMKDYMGKISKESKFLDVLVELEKLNVAPODLLEKCL 60
 DB 97 MAIGEDLDKSDVSLIFLMKDYMGKISKESKFLDVLVELEKLNVAPODLLEKCL 156
 QY 61 KNHRIIDLTKTKIQKXKQSVQAGTSYRNVLOAATOKSLKDPNNR----- 106
 DB 157 KNHRIIDLTKTKIQKXKQSVQAGTSYRNVLOAATOKSLKDPNNRFLHNGSKKQRLKEQ 216
 QY 107 -----EERPKKSTIOESAFLPQSIPEERYKMKSPGLICLIIDICINETELLADPTFTSLGY 162
 DB 217 LGAQEPVKKSIOESAFLPQSIPEERYKMKSPGLICLIIDICINETELLADPTFTSLGY 276
 QY 163 EVQKFLHLSHGISOILGQFACMPEHRDYSFVCVLVSRGSGSVYGVQTHSGPLPHI 222
 DB 277 EVQKFLHLSHGISOILGQFACMPEHRDYSFVCVLVSRGSGSVYGVQTHSGPLPHI 336
 QY 223 RRMFMDSCPYLAGKPKFFIIONVYVSDGQLEDSLLLEVDPAMKNVEFFKQKRGCTVH 282
 DB 337 RRMFMDSCPYLAGKPKFFIIONVYVSDGQLEDSLLLEVDPAMKNVEFFKQKRGCTVH 396
 QY 283 READPFMSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
 DB 397 READPFMSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435

RESULT 14
 US-09-935-223-2
 ; Sequence 2, Application US/09935223
 ; Publication No. US20020086983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altemet, Ema S.
 ; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, Ar
 ; FILE REFERENCE: T02499
 ; CURRENT APPLICATION NUMBER: US/09/935,223
 ; CURRENT FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 09/723,450
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/726,993
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 08/859,167
 ; PRIOR FILING DATE: 1997-05-20
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 445
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Novel Sequence
 ; US-09-935-223-2

Query Match 86.4%; Score 1554.5; DB 12; Length 445;
 Best Local Similarity 94.4%; Pred. No. 1.2e-145;
 Matches 309; Conservative 1; Mismatches 0; Indels 17; Gaps 1;
 QY 1 MAIGEDLDKSDVSLIFLMKDYMGKISKESKFLDVLVELEKLNVAPODLLEKCL 60
 DB 97 MAIGEDLDKSDVSLIFLMKDYMGKISKESKFLDVLVELEKLNVAPODLLEKCL 156

QY 61 KNHRIIDLTKTKIQKXKQSVQAGTSYRNVLOAATOKSLKDPNNRFEERPKKSTIOESAF 120
 DB 157 KNHRIIDLTKTKIQKXKQSVQAGTSYRNVLOAATOKSLKDPNNR----- 202
 QY 121 LPQSIPEERYKMKSPGLICLIIDICINETELLADPTFTSLGYEQKFLHLSHGISOILG 180
 DB 203 -----SIPEERYKMKSPGLICLIIDICINETELLADPTFTSLGYEQKFLHLSHGISOILG 259
 QY 181 QFACMPEHRDYSFVCVLVSRGSGSVYGVQTHSGPLPHIRRMFMDSCPYLAGKPKM 240
 DB 260 QFACMPEHRDYSFVCVLVSRGSGSVYGVQTHSGPLPHIRRMFMDSCPYLAGKPKM 319
 QY 241 FFIIONVYVSDGQLEDSLLLEVDPAMKNVEFFKQKRGCTVHREADPFMSLCTADMSLLE 300
 DB 320 FFIIONVYVSDGQLEDSLLLEVDPAMKNVEFFKQKRGCTVHREADPFMSLCTADMSLLE 379
 QY 301 QSHSSPSLYLOCLSQKLRQER 321
 DB 380 QSHSSPSLYLOCLSQKLRQER 400

RESULT 15
 US-09-410-194-12
 ; Sequence 12, Application US/09410194
 ; Patent No. US20020095030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Techopp, Jurg
 ; APPLICANT: Thome, Margot
 ; APPLICANT: Burns, Kimberly
 ; APPLICANT: Imtler, Marten
 ; APPLICANT: Hahne, Michael
 ; APPLICANT: Schroter, Michael
 ; APPLICANT: Schneider, Pascal
 ; APPLICANT: Bodmer, Jean- Luc
 ; APPLICANT: Steiner, Veronique
 ; APPLICANT: Rimoldi, Donata
 ; APPLICANT: Holmann, Kay
 ; APPLICANT: French, E. Lars
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
 ; FILE REFERENCE: 11141-002001
 ; CURRENT APPLICATION NUMBER: US/09/410,194
 ; CURRENT FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01857
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
 ; PRIOR FILING DATE: 1997-04-01
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 481
 ; TYPE: PRF
 ; ORGANISM: Mus musculus
 ; US-09-410-194-12

Query Match 56.6%; Score 1018; DB 9; Length 481;
 Best Local Similarity 62.6%; Pred. No. 3.6e-92;
 Matches 211; Conservative 41; Mismatches 67; Indels 18; Gaps 5;

QY 1 MAIGEDLDKSDVSLIFLMKDYMGKISKESKFLDVLVELEKLNVAPODLLEKCL 60
 DB 102 LMEIGESLDQNDVSLVFLTRDYGRKIAKDSFLDVLVELEKLNVAPODLLEKCL 161
 QY 61 KNHRIIDLTKTKIQKXKQSVQAGTSYRNVLOAATOKSLKDPNNR-----NNFRFP----- 109
 DB 162 KNHRIIDLTKTKIQKXKQSVQAGTSYRNVLOAATOKSLKDPNNR-----NNFRFP----- 220
 QY 110 -----VKKSIOESAFLPQSIPEERYKMKSPGLICLIIDICINETELLADPTFTSLGYEV 164
 DB 221 SQRTLVKTSIOESGAFLPPIHIREIRYMQSKPLGICLIIDICIGDITVLOKTFFTSLGYHI 280
 QY 165 QKFLHLSHGISOILGQFACMPEHRDYSFVCVLVSRGSGSVYGVQTHSGPLPHIRR 224

Db	281	QLFLPKSHDITQIVRRYASMAQHQDYDSFACVLVSLGSGQSMGRDQVHSGFSLDHYKN	340
Qy	225	MFWDSCPYLAGKPKMFPIQNYVVDGQLEDSSILEVDGPAMKNVEFKAQKRGCTVHRE	284
Db	341	MFTGDTCPSLRGKPKLFFIQNYESLGSQLEDSS-LEVDPSPINVDSKPLQPRHCTTHPE	399
Qy	285	ADFFMSLCTADMSLLEQSHSPSLYLQCLSOXLROER	321
Db	400	ADFFMSLCTADVSHLEKPSSSSVYLOKLSQULKQGR	436

Search completed: September 8, 2004, 06:22:25
Job time : 1043 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 ; Search time 19 Seconds
(without alignments)
1761.824 Million cell updates/sec

Title: US-10-713-208-6

Sequence: 1 MAEIGEDLKSDVSSLIPLM.....ITRSKDWPFSSUGCTILDVL 348
Perfect score: 1800

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	184.5	10.2	212	2	167437	cysteine proteinase
2	184.5	10.2	277	2	S64710	cysteine proteinase
3	184.5	10.2	277	2	UC5410	CPP32 protein - mouse
4	183.5	10.2	277	2	AS5315	cysteine proteinase
5	180.5	10.0	452	2	JC6507	caspase-2 - rat
6	177.5	9.9	435	2	AS4821	apoptosis regulator
7	169	9.4	312	2	BS4821	apoptosis regulator
8	161	8.9	416	2	G02635	ICB-LAP6 - human
9	149.5	8.3	182	2	167436	interleukin-1-beta
10	138.5	7.7	418	2	B57511	interleukin-1-beta
11	136	7.6	383	2	AS6084	interleukin-1-beta
12	134	7.4	454	2	TC7123	caspase-9 long chain
13	129.5	7.2	495	2	T20038	hypothetical prote
14	129.5	7.2	503	2	A49429	interleukin-1-beta
15	126.5	7.0	404	2	A42677	interleukin-1-beta
16	124.5	6.9	311	2	B56084	interleukin-1-beta
17	122	6.8	241	2	T30761	hypothetical prote
18	120	6.7	263	2	CS6084	interleukin-1-beta
19	116	6.4	377	2	AS7511	interleukin-1-beta
20	109.5	6.1	402	2	A46495	IL-1 beta converta
21	102	5.7	1537	2	F86509	CT147 hypothetical
22	102	5.7	1537	2	C81558	conserved hypothet
23	102	5.7	1537	2	H72112	ct147 hypothetical
24	101.5	5.6	743	2	G83726	assimilatory nitrate
25	100	5.6	1819	2	A71928	cag island protein
26	98.5	5.5	613	2	A99552	oligodeopeptidase
27	98.5	5.5	680	2	T41670	hypothetical zinc
28	98.5	5.5	1641	2	T10955	early nodulin bind
29	97.5	5.4	854	2	C83905	hypothetical prote

30	97.5	5.4	2104	2	T18774	myosin-3 heavy cha
31	97	5.4	892	2	AG1661	transcription regu
32	96.5	5.4	1287	2	T42658	hypothetical prote
33	96	5.3	488	2	T13385	hypothetical prote
34	95	5.3	892	2	A11289	transcription regu
35	95	5.3	1629	2	T06461	DNA-binding protei
36	94.5	5.2	344	2	B70136	flagellar motor sw
37	94	5.2	1713	2	A55347	adhesive ligand ep
38	94	5.2	2670	2	A45719	inositol 1,4,5-tri
39	94	5.2	2671	2	A49873	inositol 1,4,5-tri
40	94	5.2	4589	2	T14914	dynein beta heavy
41	93.5	5.2	1811	2	T39252	probable protein t
42	93	5.2	455	2	G70113	replicative DNA he
43	93	5.2	1265	2	T47626	structural mainten
44	93	5.2	1875	2	S38173	myosin-like protei
45	93	5.2	1927	2	G64585	cag pathogenicity

ALIGNMENTS

RESULT 1

167437

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C/Accession: 167437

R/Flaws: J.A.; Kugu. K.; Trbovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Til

A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel

A/Reference number: 153300; PMID:96042508; PMID:7588240

A/Accession: 167437

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1212 <RES>

A/Cross-references: EMBL:U34685; NID:g1004370; P1DN:AAC52251.1; P1D:g1004371

C/Keywords: cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 212;
Best Local Similarity 29.1%; Pred. No. 7.2e-07;
Matches 60; Conservative 36; Mismatches 81; Indels 29; Gaps 8;

QY	127	EEHYKMKSKPLGICLIID-----CIGNETL---LRDTSTSGYEQKRLHISM	172
DB	5	DSSEYKMDYDEMGLCIINNNKFNKSTGMSARRNGTVDANLRETFWALKYERNNKNDLTR	64
QY	173	HGISOILGCPACPEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLRHHIRRMFGDSCP	232
DB	65	EEIMELMDSVS-KEDSKSSSFVCVILSHGDEGVIFG---TNGPVDIKKLISFFRGDYCR	120
QY	233	YLAKPRMFFIQNYVVSQQLDSDSLLEVDPKMKNVKFAKQKGLCTVHRPADFFWSLC	292
DB	121	SLTGKPKLFTFIQ---ACRGTEIDSG-IETDSGADDDV--ACCKKRV-----EADFLVAYS	169
QY	293	TADMSLEQSHSSPSLYLQCLSGKLR	318
DB	170	SAPGYISWKRSGSWFIQSLCMLK	195

RESULT 2

S64710

C/Species: Citellus griseus (Chinese hamster)

C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C/Accession: S64710; S72395

R/Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.

EMBO J. 15, 1012-1020, 1996

A/Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during

A/Reference number: S64710; PMID:96183185; PMID:8605870

A/Accession: S64710

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A:Residues: 1-277 <MAN>
 A:Cross-references: EMBL:U27463
 R:Wang, X.
 Submitted to the EMBL Data Library, May 1995
 A:Reference number: S72395
 A:Accession: S72395
 A:Molecule type: mRNA
 A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <MAN>
 A:Cross-references: EMBL:U27463; NID:G1244443; PIDN:AA01511.1; PID:G1244444
 C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 27.9%; Pred. No. 1e-06;
 Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

QY 96 KSLKPPNNPREPYKKS-IOESAPLPQSIPEERYKSKPLGICLIID----- 144
 DB 11 KSIK---NFEVKTIHSGSKMSDGIYDSS---YKMDYPEMGVCIINNNKPKHSTGM 61
 QY 145 --CIGNETEL--LSDFTSLGYEVOKFLHSMHGISOILGQFACMPBHRDYDSFVCVLVS 200
 DB 62 TPRSTVDPAKLETFTNKLKYEVANKNDLTREIYVLM-KAKSKEDHSKRSFVCVLVS 120
 QY 201 RGGSGSYGVQDTHSGPLHHRFMFGDSCPYLAGKPKKFFIQ--NYVSDGQLEDSS 258
 DB 121 HDEGVIRPGTD---GPIDLKLTGYFRGDCRSRLTGKPKLFIQACRGTELDGIEITDSG 177
 QY 259 LEVDGPAKKNVEFKAKRGCLTVHREADPFMSLCTADMSLLEQSHSPSLYLQCSQKLR 318
 DB 178 TEDMTCK-----IPEADFLYAVSTAGYYSWRNPKDGSWFIQSLCMLK 224

RESULT 3
 JC5410
 C:P32 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
 C:Accession: JC5410
 R:Okada, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 Biochem. Biophys. Res. Commun. 231, 770-774, 1997
 A:Title: Specific expression of C/P32 in sensory neurons of mouse embryos and activation
 A:Reference number: JC5410; MUID:97224429; PMID:9070890
 A:Accession: JC5410
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-277 <MOK>
 A:Cross-references: DDBJ:D86352
 A:Experimental source: embryo
 C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 28.9%; Pred. No. 1e-06;
 Matches 67; Conservative 35; Mismatches 93; Indels 37; Gaps 11;

QY 103 NNPREPY--KKSIOESAPLPQSIPEERYKSKPLGICLIIT-----DCIGN 148
 DB 14 NNFGVKTTHGSKSY-DSGIYDSS-----YKMDYPEMGICIIITNNKPKHSTGMSSRSGT 67
 QY 149 ETEL--LSDFTSLGYEVOKFLHSMHGISOILGQFACMPBHRDYDSFVCVLVSRRGSGS 206
 DB 68 DVDANLLETFTMGKLYEVANKNDLTREIYVLMDSV-KEDHSKRSFVCVLVSHGDEGV 126
 QY 207 VYGVDQTHSGPLHHRFMFGDSCPYLAGKPKKFFIQNVVSDGQLEDSSLLEVDGPAK 266
 DB 127 IFG---TNGPVDLKLTGYFRGDCRSRLTGKPKLFIQ--ACRGTELDG-IEITDSGT- 178
 QY 267 KNVEFKAKRGCLTVHREADPFMSLCTADMSLLEQSHSPSLYLQCSQKLR 318
 DB 179 -DEMAQCK-----IPEADFLYAVSTAGYYSWRNPKDGSWFIQSLCMLK 224

RESULT 4
 A55315

cysteine proteinase (EC 3.4.22.-) C/P32 precursor - human
 N:Alternate names: cysteine proteinase C/P32

C:Species: Homo sapiens (man)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
 C:Accession: A55315; S58899; I39005
 R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
 J. Biol. Chem. 269, 30761-30764, 1994

A:Title: C/P32, a novel human apoptotic protein with homology to Caenorhabditis elegans
 A:Reference number: A55315; MUID:95074098; PMID:7983002
 A:Accession: A55315

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-277 <FPR>
 A:Cross-references: GB:U13737; NID:G561665; PIDN:AAA65015.1; PID:G561666
 R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant,
 J.; Yu, V.L.; Miller, D.K.
 Nature 376, 37-43, 1995

A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mamma
 A:Reference number: S58899; MUID:95319529; PMID:7596430
 A:Accession: S58899

A:Molecule type: protein
 A:Residues: 29-46,176-189, 'E', 191-193 <NIC>
 R:Reichert, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poit
 Cell 81, 801-809, 1995

A:Title: Yama/C/P32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
 A:Reference number: A56924; MUID:95292347; PMID:7774019
 A:Accession: I39005

A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-189, 'E', 191-277 <RBS>
 A:Cross-references: EMBL:U26943; NID:G857568; PIDN:AAV4929.1; PID:G857569
 C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 10.2%; Score 183.5; DB 2; Length 277;
 Best Local Similarity 26.4%; Pred. No. 1.2e-06;
 Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

QY 98 LKDPNNPREPYK--KSIOESAPLPQSIPEERYKSKPLGICLIID----- 144
 DB 1 MENTENSVVSQSKSKNLEPKTIHSGSEMSDGLSDSYKMDYPEMGLCIINNNKPKHSTG 60
 QY 145 ---CIGNETEL--LSDFTSLGYEVOKFLHSMHGISOILGQFACMPBHRDYDSFVCVLV 199
 DB 61 MTRSGTDVPAKLETFTNKLKYEVANKNDLTREIYVLMDSV-KEDHSKRSFVCVLV 119
 QY 200 SRGSGSYGVQDTHSGPLHHRFMFGDSCPYLAGKPKKFFIQ--NYVSDGQLEDSS 257
 DB 120 SHGEGHIFG---TNGPVDLKLTGYFRGDCRSRLTGKPKLFIQACRGTELDGIEITDS 176
 QY 258 LLEVDGPAKKNVEFKAKRGCLTVHREADPFMSLCTADMSLLEQSHSPSLYLQCSQKLR 317
 DB 177 GVDDDMACHK-----IPEADFLYAVSTAGYYSWRNPKDGSWFIQSLCML 223
 QY 318 RQ 319
 DB 224 KQ 225

RESULT 5
 JC6507
 caspase-2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: JC6507
 R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
 Gene 202, 127-132, 1997
 A:Title: Cloning and expression of the cDNA encoding rat caspase-2.
 A:Reference number: JC6507; MUID:98087427; PMID:9427555
 A:Accession: JC6507
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-452 <SAT>
 A:Cross-references: GB:U79933; NID:G2769705; PIDN:AA096379.1; PID:G2769706

Query Match 10.0%; Score 180.5; DB 2; Length 452;
Best Local Similarity 21.3%; Pred. No. 4,1e-06;
Matches 86; Conservative 60; Mismatches 137; Indels 121; Gaps 14;

42 LEKLNIVARDQ---DLLEKCL-KNIHRIDLKTKIQ---KYKQSVQAGTSYRNVLQA- 92
Db LKKNRVYLAQKQLLSLEHLEKDIITLEMRELIQAQKGSFSQVLELNLTPKRGQA 99
40 LKKNRVYLAQKQLLSLEHLEKDIITLEMRELIQAQKGSFSQVLELNLTPKRGQA 99
QY -AIOKSLKDPNSNNFRBPVKKSIOESEALP-----QSIPEER----- 129
Db 100 DAFCEALRETRQGHLEDMILITLISDIOHILPPLSCDYDLSLFPVCESCPPIKQSRUSTD 159
QY 130 -----YKMKSKPLGICLIIDCI----- 146
Db 160 TWEHSLDNKGDPVCLQVPCPTPEFYQTHQOLAYRLQSQPRGIALVMSVHFTEKDELEFR 219
QY 147 -GNETE--LIRDFTSLGYEVQKFLHLSMHGISOILIGQFACMPERHDYDSCVCLVSRGG 203
Db 220 SGGDVHSTLVTLFPLKLGYNVHVLCDQTAQOEQEKLONFQAQPAHRYVDSCTVALLSHGV 279
QY 204 SGSVYGVDTGHSGLPLHNRMRMGDSCPYLAKGPKMFFIQ-----NY 246
Db 280 EGGITGYVD--GKLLQIQEVFRLFDNANCPSLQNKPKMFFIQCRGDETRDGVQDDGKNH 337
QY 247 VVSDGQLEBSS---LLEVDGPMK-----NVEFKQKRGCLTVHREADFPMSL 291
Db 338 AQSFGCEESDPAGEELMKRMELPTRSDMIGVACLKKNAMRNTKSGSVYIETALTQVF--SE 396
QY 292 CTADMSLLESHSFSPLYQCLSQKLRQERGTIPSGITESKDM 335
Db 397 RACDMHVADM-----LVKNALTKEREGYAFGEFRCKEM 432

RESULT 6
A54821
apoptosis regulator ICH-1, stimulatory form L - human
C/Species: Homo sapiens (man)
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C/Accession: A54821
R/Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A/Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
A/Reference number: A54821; MUID:94373811; PMID:8087842
A/Accession: A54821
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-435 <MAN>
A/Cross-references: GB:U10321; NID:9537291; PID:9537292
C/Keywords: alternative splicing; apoptosis

Query Match 9.9%; Score 177.5; DB 2; Length 435;
Best Local Similarity 20.6%; Pred. No. 6,6e-06;
Matches 82; Conservative 62; Mismatches 145; Indels 109; Gaps 12;

42 LEKLNIVARDQ---DLLEKCL-KNIHRIDLK---TKIQKQSVQAGTSYRNVLQA- 92
Db 23 LKKNRVYLAQKQLLSLEHLEKDIITLEMRELIQAQKGSFSQVLELNLTPKRGQA 82
QY 93 -AIOKSLKDPNSNNFRBPVKKSIOESEALP-----QSIPEER----- 126
Db 83 DAFCEALRETRQGHLEDMILITLISGQHVLPPLSCDYDLSLFPVCESCPPIKQSRUSTD 142
QY 127 -----EERYKMKSKPLGICLIIDCI--GNETE--- 152
Db 143 TWEHSLDNKGDPVCLQVPCPTPEFYQTHQOLAYRLQSQPRGIALVMSVHFTEKDELEFR 202
QY 153 -----LIRDFTSLGYEVQKFLHLSMHGISOILIGQFACMPERHDYDSCVCLVSRGG 203
Db 203 SGGDVHSTLVTLFPLKLGYNVHVLCDQTAQOEQEKLONFQAQPAHRYVDSCTVALLSHGV 262
QY 204 SGSVYGVDTGHSGLPLHNRMRMGDSCPYLAKGPKMFFIQVYVSDGLEBSSLLEVDG 263

Db 263 EGAITGYVD--GKLLQIQEVFQLFDNANCPSLQNKPKMFFIQ---ACRGDETRDGVQDDG 317
QY 264 -----PANKVVEFAQKRGCLTVHREADFPMSLCTADMSLLEQSHSSPPLYLOCLSQ-- 315
Db 318 KHNASSPGCEESDACKELPKRRLPTRSDMIGVACLKGTANMNTKRGSVYIETALTQVF 377
QY 316 -----KLROERGTPGSGITESKDM 335
Db 378 SERACDMHVADMVLKVNALIKDRBEGVAPGTGEFRCKEM 415

RESULT 7
B54821
apoptosis regulator ICH-1, suppressive form S - human
C/Species: Homo sapiens (man)
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C/Accession: B54821
R/Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A/Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
A/Reference number: A54821; MUID:94373811; PMID:8087842
A/Accession: B54821
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-312 <MAN>
A/Cross-references: GB:U10322
C/Keywords: alternative splicing; apoptosis

Query Match 9.4%; Score 169; DB 2; Length 312;
Best Local Similarity 23.5%; Pred. No. 1,9e-05;
Matches 66; Conservative 45; Mismatches 90; Indels 80; Gaps 9;

42 LEKLNIVARDQ---DLLEKCL-KNIHRIDLK---TKIQKQSVQAGTSYRNVLQA- 92
Db 9 LKKNRVYLAQKQLLSLEHLEKDIITLEMRELIQAQKGSFSQVLELNLTPKRGQA 68
QY 93 -AIOKSLKDPNSNNFRBPVKKSIOESEALP-----QSIPEER----- 126
Db 69 DAFCEALRETRQGHLEDMILITLISGQHVLPPLSCDYDLSLFPVCESCPPIKQSRUSTD 128
QY 127 -----EERYKMKSKPLGICLIIDCI--GNETE--- 152
Db 129 TWEHSLDNKGDPVCLQVPCPTPEFYQTHQOLAYRLQSQPRGIALVMSVHFTEKDELEFR 188
QY 153 -----LIRDFTSLGYEVQKFLHLSMHGISOILIGQFACMPERHDYDSCVCLVSRGG 203
Db 189 SGGDVHSTLVTLFPLKLGYNVHVLCDQTAQOEQEKLONFQAQPAHRYVDSCTVALLSHGV 248
QY 204 SGSVYGVDTGHSGLPLHNRMRMGDSCPYLAKGPKMFFIQ 244
Db 249 EGAITGYVD--GKLLQIQEVFQLFDNANCPSLQNKPKMFFIQ 287

RESULT 8
G02635
ICE-LAP6 - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C/Accession: G02635
R/Duan, H.; O'Connell, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
submitted to the EMBL Data Library, April 1996
A/Reference number: H01513
A/Accession: G02635
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1416 <DUA>
A/Cross-references: EMBL:U56380; NID:g1336026; PID:NA050640.1; PID:g1336027

Query Match 8.9%; Score 161; DB 2; Length 416;
Best Local Similarity 22.0%; Pred. No. 0,00011;
Matches 77; Conservative 60; Mismatches 149; Indels 64; Gaps 11;

QY 19 LMDVNGRGKISNFKSLDVLVVELEKLNIVARDQDLLEKCLKNIHRIDLKTKIQKQSV 78

```

Db      39 MIEDIQRAGSSRRDQARQLIIDLETRGSA---LPLFISCLDTEQDMLASLRNRQA 95
Qy      79 VQAGTGYRNLQALICSLKDP-----SNNFREPPYKKSIOSEAFPLPQS 124
Db      96 GKLSTKPTLENLTPVLAKEIKPEVLAPEPRPVADISGGFGVGVALSIRGN----- 148
Qy      125 IPEERYKKSKPLGLICLIIDCTG--NTELLRDTFTSLGYEVQKFLHLSMEGISQLGCF 182
Db      149 ADLAVYLISMPEPCGHCILINNVNFCRESGLRTRGNSIDEXKLRFRFSSLHFVEVKGDL 207
Qy      153 A-----CMPEHRDYSFVCLVSRGSGS-----YVGQDQTHSGLP--LHHI 222
Db      208 TAKKMYVLLBELAQDHGALDCCVAVILSHGCQASHLQFPAVYGTD---GCPVSEVKI 263
Qy      223 RRMFKGDCSPYLAGKPKMFQ-----NYVSDQLED---SLLEVDG-PAMKNV 269
Db      264 VNIFGTCSPSLGKPKLFIQACGGEQKHGEFVASTPDEBSPGSPNPEPDATPQEG 323
Qy      270 EFKQKRGCLCTVHREADPFMSLCTADMSLLEQSHSSSLYLQCLSQKLAQ 319
Db      324 RFPQDLAISSLPTPSDIFVYSYTFPGFVSMRDPKSGSWYETLDDIFEQ 373

```

RESULT 9

```

167436 Interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C/Accession: 167436
R/Flaws, J.A.; Kugui, K.; Tirovich, A.M.; Desanti, A.; Tilly, K.I.; Hershfield, A.N.; Til
A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nucleo cells of the ovarian follicle
A/Reference number: 153300; MUID:96042508; PMID:7588240
A/Accession: 167436
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-182 <RES>
A/Cross-references: EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g1004369

```

Query Match 8.3%; Score 149.5; DB 2; Length 182;

Best Local Similarity 31.0%; Pred. No. 0.00028;

Matches 44; Conservative 18; Mismatches 61; Indels 19; Gaps 4;

```

Qy      136 PLGICLIDCI-----GNFTE--LIRDFTSLGVEYQKFLHLSMGISQILCQ 181
Db      1 PRGLALVMSNVHFTGEXDLERPGSDVDHTLVTLFRLGLGVNHNVLVYDQTAGEMEKLN 60
Qy      182 PACPEHRDYSFVCLVSRGSGSYGVQDQTHSGLPPLHIRMFKGDCSPYLAGKPKMF 241
Db      61 FAQIPARHVTDSCTVALSHGVEGIGYVD--GKLQLQDEVFLFDNANCPSLONKPKMF 118
Qy      242 FIGNVYVSDGLEDSLLEVDG 263
Db      119 FIQ--ACRGDETGRGVQDDG 137

```

RESULT 10

```

B57511 Interleukin-1 beta converting enzyme (EC 3.4.22.-) ICErel-III - human
C/Species: Homo sapiens (man)
C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 01-Dec-2000
C/Accession: B57511; S62183
R/Flaws, N.A.; Vaillancourt, J.P.; Ali, A.; Casano, F.J.; Miller, D.K.; Mollineux, S.M.
J. Biol. Chem. 270, 15870-15876, 1995
A/Title: Molecular cloning and pro-apoptotic activity of ICE-relIII and ICE-relIII, membe
A/Reference number: A57511; MUID:95318183; PMID:7797592
A/Accession: B57511
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-418 <MND>
A/Cross-references: GB:U28015; NID:g975300; PIDN:AAV5172.1; PID:g903936

```

```

R/Faucheu, C.; Blanchet, A.M.; Collard-Ducilleul, V.; Lalanne, J.L.; Du-Hercend, A.
Eur. J. Biochem. 236, 207-213, 1996
A/Title: Identification of a cysteine protease closely related to interleukin-1-beta-c
A/Reference number: S62183; MUID:95184899; PMID:8617266
A/Accession: S62183
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 55-317; V, 319-418 <PAU>
A/Cross-references: EMBL:X54993; NID:g1155085; PIDN:CAA64450.1; PID:g1155086
C/Keywords: cysteine proteinase; hydrolase

```

Query Match 7.7%; Score 138.5; DB 2; Length 418;

Best Local Similarity 23.4%; Pred. No. 0.006;

Matches 77; Conservative 52; Mismatches 125; Indels 75; Gaps 16;

```

Qy      10 KSDVSLIPLMD-----YMGKG---KISKEKSLDLVLELEKUNLVAPQDLLE 57
Db      50 KKTVMKLEVLGKDVHGVFNVLAKHDVLTLKEEKKKKYYDAKIEDKALILV-----DSL 104
Qy      58 KCLKNHRIDLKTKQKYGQSVQAGTGYRNLQALICSLKDPNNF-----REPPYK 112
Db      105 K-NVAAHQFTQT-LINMDQKI---TSVKPLQIEAGPEPASAETNLKLCPEEERL 158
Qy      113 SIOSEAFPLPOSIPERYKKSKPLGICLI-----DCIGNETELRDT 156
Db      159 CKQNDHEIVPIKKREDRR-----LALLICNTKFDHLPARNGAHYDIVG-----MKRL 206
Qy      157 FTSLGVEYQKFLHLSMGISQILGOFACMPEHRDYSFVCLVSRGSGSYGVQ--DQT 213
Db      207 LQGLGTVVDKXKTLIRDMESVLRAPAAPEKSSDSFTLVMSHGILEGICGTAHKKK 266
Qy      214 HSGLPPLHIRMFKGDCSPYLAGKPKMFQYVSDQ-----LEDS--SLLEVDGPA 265
Db      267 PDLVLDITFQIFNNNCISLMDKPKVLIYQ--ACREKKGELVWRSPASLAVISGS 323
Qy      266 MKQVFPKQKRGCLCTVHREADPFMSLCTA 294
Db      324 SENLEADS---VCKIHEKDFI-AFCS 347

```

RESULT 11

```

A56084 Interleukin-1beta converting enzyme beta isozyne - human
C/Species: Homo sapiens (man)
C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
C/Accession: A56084
R/Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A/Title: Cloning and expression of four novel isoforms of human interleukin-1beta conv
A/Reference number: A56084; MUID:95181414; PMID:7876192
A/Accession: A56084
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-383 <ALN>
A/Cross-references: GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040
C/Genetics:
A/Gene: IL1BC3
C/Keywords: alternative splicing

```

Query Match 7.6%; Score 136; DB 2; Length 383;

Best Local Similarity 24.0%; Pred. No. 0.0083;

Matches 61; Conservative 54; Mismatches 145; Indels 58; Gaps 12;

```

Qy      24 MGRGKTSKESFLDLVLELEKUNLVAPQDLLEKLNHRIDKTKYQKYSQV--- 80
Db      17 MGRGGIN---GLDELDTQTRVANKMEKVENKYNATVMDKTRALIDSVIFGAACQIC 73
Qy      81 -----GAGSYRNLQALICSLKDPSPNFEPPYK-SIOSEAFPLPOSIPERY 130
Db      74 TYICEDSYLAGTGLISAPQAVQDNPPAMPTSSGSEGVKCLSEAPGRIMKQKSAETYP 133
Qy      131 KM-KSRPLGICLI-----DCI-----GNTELLRDT--FTSLGVEYQKFLHLSMGISQI 178

```

Db 134 IMDSKSRRLALLICNEEPDSIPRTGAEDVITGMMLLONTLGYSVDYKKNLTASDMTE 193
Cy 179 LGFACMCPEHRDSDPFCVLYSRGSGOSVYG--VQOTSGPLHHIRMFMGDSCEPLA 235
Db 194 LEAFARPEKHTDSTFLVMSHGIRGICGKKHSQVDDIIQLNMFMTNTKCPSELK 253
Cy 236 GKRPMEFIQ-----NYVSDQLEDSDSLLLEVDPAMKNVBEKAKRGICLCTVH 282
Db 254 DKRPVITIQACRGDSPGVWFVKDSVSGNLSLPTFEFEDAIKK-----AH 301
Cy 283 READPFWSLCTADMSLLEQSH--SSPLYLQCLSQKLRQ 319
Db 302 IEKDFI-AFCSSTPDNVSRHPTMGVSGFIRGLEHMOE 338

RESULT 12

JC7123

Caspase-9 long chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001

C:Accession: JC7123

R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.

Biochem. Biophys. Res. Commun. 264, 550-555, 1999

A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.

A:Reference number: JC7123; MUID:20001956; PMID:10529400

A:Accession: JC7123

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-454 <FUJ>

A:Cross-references: DDBJ:AB019600; NID:G6440941; PID:G6440942

Query Match 7.4%; Score 134; DB 2; Length 454;

Best Local Similarity 33.1%; Pred. No. 0.015;

Matches 45; Conservative 15; Mismatches 52; Indels 24; Gaps 6;

Cy 130 YKMSKPLGICLIID-----IGNET-----ELLDFTSLGYEVQKFLHSMGI 175
Db 191 YTLDSDCGCHLIINNNPFRSSGGLCTRCSNIDRKLHRRMLRFMEVGNLDLTKKM 250
Cy 176 SQTIGFACMCPEHRDSDPFCVLYSRGSGOS-----YGVQDQHSGLPLHIRMENG 228
Db 251 VTALMEWA-HRNRALDCFVVVILSHGCCQASHLQPGAVYGTD--GCSYSIEKIYINENG 307

Cy 229 DSCPYLAGKRPMEFIQ 244
Db 308 SCGSPSLGKRPKLFPIQ 323

RESULT 13

T20038

hypotheoretical protein Ca4D1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20038

R:Burton, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19214

A:Accession: T20038

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-495 <WIL>

A:Cross-references: EMBL:Z81049; PIDN:CA802848.1; GSPDB:GN00022; CESP:CA8D1.2

A:Experimental source: clone CA8D1

C:Genetics:

A:Gene: CESP:CA8D1.2

A:Map position: 4

A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 7.2%; Score 129.5; DB 2; Length 495;

Best Local Similarity 24.0%; Pred. No. 0.037;

Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

Cy 70 TKIOXKQSVQAGTSRYNVLQAIQKS-----LKDPNNPREP----- 109

Query Match 7.2%; Score 129.5; DB 2; Length 495;

Best Local Similarity 24.0%; Pred. No. 0.037;

Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

Cy 70 TKIOXKQSVQAGTSRYNVLQAIQKS-----LKDPNNPREP----- 109

Db 125 TRYHRDSVSVSFTYQDIYSRARSRSRALHSSDRHNSPFPVNAFPSPSSANSS 184
Cy 110 -----VKKSIQSEAPLPQSTPEE-----RYKMSKPLGIC 140
Db 185 TGCSSLIGYSSRRRSFKASGPTQYIFHEEDNFPVADPTISRVEDEKTYNFPSPRCMC 244
Cy 141 LIID-----CIGNTELLRDTFTSL-----GYEVQKFLHSMHGISQILQFACMCPEHR 189
Db 245 LINNEHFQMPFRNCTKADKDNLTNLPFCMGVTVICKDNLTGRGMLLTIRDF--KHE 301
Cy 190 DY-DSFVCVLYSRGSGOSVYGVQDQHSGLPL--HHIRKFMDSQCPYLAGKRPMEFIQNY 246
Db 302 SHGDSALIVLSHGENVILIGVD-----IPSTHEIYDLNNAANPRLANKRIVFVQ-- 355
Cy 247 VVSDQLEDSDS---LLEVDP-PA 265
Db 356 -ACRGERRDNGFPVLDSVDGVA 377

RESULT 14

A49429

interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A49429; T37312

R:Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.W.; Horvitz, H.R.

Cell 75, 641-652, 1993

A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int

A:Reference number: A49429; MUID:94061982; PMID:8242740

A:Accession: A49429

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-503 <YUA>

A:Cross-references: GB:L29052; NID:G6503233; PIDN:AAA27982.2; PID:G6503233

A:Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBI:139826)

C:Genetics:

A:Gene: ced-3

A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 463/3

Query Match 7.2%; Score 129.5; DB 2; Length 503;
Best Local Similarity 24.0%; Pred. No. 0.038;

Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

Cy 70 TKIOXKQSVQAGTSRYNVLQAIQKS-----LKDPNNPREP----- 109
Db 126 TRYHRDSVSVSFTYQDIYSRARSRSRALHSSDRHNSPFPVNAFPSPSSANSS 185
Cy 110 -----VKKSIQSEAPLPQSTPEE-----RYKMSKPLGIC 140
Db 186 TGCSSLIGYSSRRRSFKASGPTQYIFHEEDNFPVADPTISRVEDEKTYNFPSPRCMC 245
Cy 141 LIID-----CIGNTELLRDTFTSL-----GYEVQKFLHSMHGISQILQFACMCPEHR 189
Db 246 LINNEHFQMPFRNCTKADKDNLTNLPFCMGVTVICKDNLTGRGMLLTIRDF--KHE 302

Cy 190 DY-DSFVCVLYSRGSGOSVYGVQDQHSGLPL--HHIRKFMDSQCPYLAGKRPMEFIQNY 246
Db 303 SHGDSALIVLSHGENVILIGVD-----IPSTHEIYDLNNAANPRLANKRIVFVQ-- 356
Cy 247 VVSDQLEDSDS---LLEVDP-PA 265
Db 357 -ACRGERRDNGFPVLDSVDGVA 378

Query Match 7.2%; Score 129.5; DB 2; Length 503;
Best Local Similarity 24.0%; Pred. No. 0.038;

Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

Cy 70 TKIOXKQSVQAGTSRYNVLQAIQKS-----LKDPNNPREP----- 109
Db 126 TRYHRDSVSVSFTYQDIYSRARSRSRALHSSDRHNSPFPVNAFPSPSSANSS 185
Cy 110 -----VKKSIQSEAPLPQSTPEE-----RYKMSKPLGIC 140
Db 186 TGCSSLIGYSSRRRSFKASGPTQYIFHEEDNFPVADPTISRVEDEKTYNFPSPRCMC 245
Cy 141 LIID-----CIGNTELLRDTFTSL-----GYEVQKFLHSMHGISQILQFACMCPEHR 189
Db 246 LINNEHFQMPFRNCTKADKDNLTNLPFCMGVTVICKDNLTGRGMLLTIRDF--KHE 302

Cy 190 DY-DSFVCVLYSRGSGOSVYGVQDQHSGLPL--HHIRKFMDSQCPYLAGKRPMEFIQNY 246
Db 303 SHGDSALIVLSHGENVILIGVD-----IPSTHEIYDLNNAANPRLANKRIVFVQ-- 356
Cy 247 VVSDQLEDSDS---LLEVDP-PA 265
Db 357 -ACRGERRDNGFPVLDSVDGVA 378

Query Match 7.2%; Score 129.5; DB 2; Length 503;
Best Local Similarity 24.0%; Pred. No. 0.038;

Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;

RESULT 15
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C:Accession: A54263; A42674; S21734; S24164

R:Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M. Genomics 20, 468-473, 1994

A:Title: Molecular characterization of the gene for human interleukin-1beta converting e

A:Reference number: A54263; MUID:94307734; PMID:8034320

A:Accession: A54263

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-404 <CE2>

A:Cross-references: GB:I27475

R:Cerretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Nese, K.; Greenstreet, T.A

Science 256, 97-100, 1992

A:Title: Molecular cloning of the interleukin-1beta converting enzyme.

A:Reference number: A42677; MUID:92229430; PMID:1373520

A:Accession: A42677

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-404 <CER>

A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:9186286

R:Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.

J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Lamjco, G.; Palyha, O.C.; Raju, S.M.; Ro

cci, M.J.

Nature 356, 768-774, 1992

A:Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proc

A:Reference number: S21734; MUID:92244338; PMID:1574116

A:Accession: S21734

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-404 <THO>

A:Cross-references: EMBL:X65019; NID:933792; PIDN:CAA46153.1; PID:933793

R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Nese, K.; March, C.J.;

Arch. Biochem. Biophys. 296, 698-703, 1992

A:Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves

A:Reference number: S24164; MUID:92337439; PMID:1321594

A:Accession: S24164

A:Status: preliminary

A:Molecule type: protein

A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>

C:Genetics:

A:Gene: GDB:111BC

A:Cross-references: GDB:132368; OMIM:147678

A:Map position: 11q23-11q23

C:Keywords: cysteine protease; hydrolase

Query Match

Best Local Similarity 7.0%; Score 126.5; DB 2; Length 404;
Matches 83; Conservative 56; Mismatches 141; Indels 79; Gaps 14;

```

QY      24 MGRGKISKESFLDLVLEKLNLPADDLLEKLNTHRIDLTKIQKYKQVQ--- 80
DB      17 MGEGRITN---GLDLBELQTRVLNKEEMEKVRENATWMDKTRALIDSVIPKGAQAQICIT 73
QY      81 -----GAGT-----SYRVNLA-----AIQSLKDPNNFREBPV 110
DB      74 TYICEDDSYLAGTGLSADQTSQNYLNMQDSQVLSFPAPQAVQDPNPAVPTSSSGSEGNV 133
QY      111 KK-STQSESAFIPQSIPEPERYKM-KSKPLGICLIT-----DCI-----GNETELLRDT--F 157
DB      134 KLCSTLEAQRITMKQSAIYIPIMDKSSRTALITICNEFFDSIPRTGAEVDTIGMTMLL 193
QY      158 TSLGEVQKFLHLSMHGISOILGQFACMPEHRDYDSFVCVLVSRGSGSQSYG--VDQTH 214
DB      194 QNLGYSVDVKQNLTPASDWTLEFAFHRPEKHTSDSTFLVFMHGIRBGICGKXSEQVP 253
QY      215 SGLPLHTRIRRMFMGSCFYLAGKXPMFFIQ-----NYVVSQQLSDSSLLLEV 261
DB      254 DILQNALPMLNKNKNSLDKPKVITIIQACRGDSRGVVPKDSVGSNLSLPTTEEF 313
QY      262 DGPAMKVEFKAQKRGCLTVHREADPFWSLCTADMSLLEQSH-SSPSLYIQCTISQKLRQ 319
DB      314 EDDAIKK-----AHIERDFT-AFCSSSTPDNVSWRHPTMGSVFGRLEEMCE 359

```

Search completed: September 8, 2004, 05:50:30
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 ; Search time 13 Seconds

(without alignments)
1393.878 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKDVSLIFLM.....ITEXKMHFSSIGCTLLDVL 348

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1635	90.8	480	1	CFLA_HUMAN
2	1006.5	55.9	484	1	CELA_MOUSE
3	313	17.4	479	1	ICB8_HUMAN
4	297	16.5	480	1	ICB8_MOUSE
5	248.5	13.8	521	1	ICB8_HUMAN
6	199	11.1	293	1	ICB6_HUMAN
7	195.5	10.9	424	1	ICB6_CHICK
8	188.5	10.5	277	1	ICB3_MOUSE
9	185.5	10.3	277	1	ICB3_RAT
10	185.5	10.3	282	1	ICB3_XENLA
11	183.5	10.2	277	1	ICB3_CRILLO
12	183.5	10.2	277	1	ICB3_HUMAN
13	179.5	10.0	435	1	ICB2_MOUSE
14	177.5	9.9	435	1	ICB2_HUMAN
15	172.5	9.6	276	1	ICB6_MOUSE
16	167.5	9.3	303	1	ICB1_HUMAN
17	167.5	9.3	312	1	ICB2_RAT
18	166	9.2	366	1	ICB8_XENLA
19	166	9.2	416	1	ICB8_HUMAN
20	163.5	9.1	303	1	ICB7_MOUSE
21	162.5	9.0	303	1	ICB7_MESAU
22	150	8.3	323	1	ICB1_DROME
23	149.5	8.3	339	1	ICB1_DROME
24	145	8.1	382	1	ICB8_XENLA
25	142.5	7.9	299	1	ICB1_SPOFR
26	138.5	7.7	418	1	ICB8_HUMAN
27	134.5	7.5	419	1	ICB6_MOUSE
28	129.5	7.2	503	1	ICB3_CAEEL
29	127.5	7.1	404	1	ICB3_PIG
30	127.5	7.1	405	1	ICB3_HORSE
31	126.5	7.0	404	1	ICB3_HUMAN
32	125.5	7.0	373	1	ICB4_MOUSE
33	124.5	6.9	410	1	ICB3_FELCA

34	122	6.8	241	1	CFLA_MOUSE	Q98325 molnucum c
35	121.5	6.8	402	1	ICB3_RAT	P43527 rattus norv
36	121	6.7	377	1	ICED_BOVIN	O75601 bos taurus
37	119.5	6.6	404	1	ICB3_CAEUV	Q9mzv7 canis fam1
38	117.5	6.5	496	1	ICED3_CAEUV	P45436 caenorhabdi
39	116	6.4	377	1	ICB4_HUMAN	P49662 homo sapien
40	109.5	6.1	402	1	ICB3_MOUSE	P29452 mus musculu
41	99.5	5.5	590	1	MP44_YLDV	Q9dhr2 yaba-like d
42	98.5	5.5	613	1	PEPF_MYCPU	Q98CP0 mycoplasma
43	97.5	5.4	2104	1	MYG3_SCHRO	O14157 schizosacch
44	96.5	5.4	1893	1	CSP2_HUMAN	Q96582 homo sapien
45	94.5	5.2	344	1	FLIG_BORBU	P52610 borrelia bu

ALIGNMENTS

RESULT 1
CFLA_HUMAN STANDARD; PRT; 480 AA.
AC O15519; O14673; O14674; O14675; O15137; O15138; O15356; O15510;
AC O43618; O43619; O43620; O60458; O60459; O60459; O9UEW1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Casp8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
DE inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casp8)
DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
DE inducer of toxicity) (MRT) (Caspase homolog) (CASH) (Inhibitor of
DE FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
DE (Bcl-2)
GN CFLAR OR CLARP OR MRT OR CASH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 13 AND 14), AND MUTAGENESIS OF
RP TYR-360.
RC TISSUE=Embryonic kidney, and Umbilical vein endothelial cells;
RX MEDLINE=97352452; PubMed=9208847;
RA Shu H.-B., Halpin D.R., Goeddel D.V.;
RT "Casp8 is a FADD- and caspase-related inducer of apoptosis.",
RL Immunity 6:751-763(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
RX MEDLINE=97470967; PubMed=9326610;
RA Har D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Trask B.J.,
RT "WRIT, a novel death-effector domain-containing protein, interacts
RT with caspases and BclXL and initiates cell death.",
RL Proc. Natl. Acad. Sci. U.S.A. 94:11335-11338(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=97360133; PubMed=9217161;
RA Immler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
RT "Inhibition of death receptor signals by cellular FLIP.",
RL Nature 388:190-195(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 8, 9 AND 10), AND MUTAGENESIS OF
RP ASP-376.
RC TISSUE=T-cell;
RX MEDLINE=97373543; PubMed=9228018;
RA Srinivasula S.M., Ahmad M., O'Connell S., Bullrich F., Banks S.,
RT "Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.",
RL J. Biol. Chem. 272:18542-18545(1997).
RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=umbilical vein endothelial cells;
 RA MEDLINE=97362203; PubMed=9211860;
 RX Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "F-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 RT CD-95-induced apoptosis.";
 RL J. Biol. Chem. 272:17255-17257(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RL Hu S., Dixit V.M.;
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE=Kidney;
 RA MEDLINE=99218584; PubMed=10200473;
 RX Rasper D.M., Vallancourt J.P., Hadano S., Houtzager V.M., Seiden I.,
 RA Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,
 RA Koop B.F., Peterson E.P., Thornberry N.A., Huang J., Macpherson D.P.,
 RA Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 RA Nicholson D.W.;
 RT "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
 RT homologue that precludes caspase-8 recruitment and activation by the
 RT CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=skin fibroblast;
 RA MEDLINE=9746025; PubMed=9289491;
 RX Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianski V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=colon carcinoma;
 RA MEDLINE=98021435; PubMed=9380701;
 RX Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "CLARP, a death effector domain-containing protein interacts with
 RT caspase-8 and regulates apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 11).
 RA MEDLINE=2110893; PubMed=11161814;
 RX Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
 RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 RA Ikeda J.-E., Hayden M.R.;
 RT "Cloning and characterization of three novel genes, AL52CR1, AL52CR2,
 RT and AL52CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
 RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
 RL Genomics 71:200-213(2001).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RA MEDLINE=22388257; PubMed=12477932;
 RX Strusberg R.U., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stagleon M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cammici P., Prange C.,
 RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Kuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywicki S.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP FUNCTION.
 RX MEDLINE=9909897; PubMed=9889531;
 RA Scaffidi C., Schmitz I., Krammer P.H., Peter M.E.;
 RT "The role of c-FLIP in modulation of CD95-induced apoptosis.";
 RL J. Biol. Chem. 274:1541-1546(1999).
 RN [13]
 RP INDUCTION.
 RX MEDLINE=99244884; PubMed=10227994;
 RA Algeciras-Schimnich A., Griffith T.S., Lynch D.H., Pava C.V.;
 RT "Cell cycle-dependent regulation of FLIP levels and susceptibility to
 RT Fas-mediated apoptosis.";
 RL J. Immunol. 162:5205-5211(1999).
 CC -1- FUNCTION: Apoptosis regulator protein which may function as a
 CC crucial link between cell survival and cell death pathways in
 CC mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
 CC apoptosis. A proteolytic fragment (p43) is likely retained in the
 CC death-inducing signaling complex (DISC) thereby blocking further
 CC recruitment and processing of caspase-8 at the complex. Full
 CC length and shorter isoforms have been shown either to induce
 CC apoptosis or to reduce TNFRSF6-triggered apoptosis. Lacks enzymatic
 CC (caspase) activity.
 CC -1- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
 CC inducing signaling complex (DISC) formed by TNFRSF6, FADD and
 CC caspase-8. A proteolytic fragment (p43) stays associated with the
 CC DISC. Also interacts with caspase-10, caspase-3, TRAF1, TRAF2 and
 CC Bcl-X(L) (in vitro).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=alternative splicing; Named isoforms=14;
 CC Name=1; Synonyms=FLIP-L, CLARP, MTRT alpha-1, CASH alpha, I-FLICE
 CC 1, FLAME-1 gamma, Usurpin alpha;
 CC IsoId=O15519-1; Sequence=displayed;
 CC Name=2; Synonyms=FLIP-S, CLARP2, MTRT beta-1, CASH beta;
 CC IsoId=O15519-2; Sequence=VSP_000828, VSP_000829;
 CC Name=3; Synonyms=MTRT alpha-2;
 CC IsoId=O15519-3; Sequence=VSP_000824, VSP_000838;
 CC Name=4; Synonyms=I-FLICE 2;
 CC IsoId=O15519-4; Sequence=VSP_000825;
 CC Name=5; Synonyms=I-FLICE 3;
 CC IsoId=O15519-5; Sequence=VSP_000840;
 CC Name=6; Synonyms=I-FLICE 4;
 CC IsoId=O15519-6; Sequence=VSP_000826, VSP_000841;
 CC Name=7; Synonyms=I-FLICE 5;
 CC IsoId=O15519-7; Sequence=VSP_000824, VSP_000827, VSP_000838;
 CC Name=8; Synonyms=Flame-1 alpha;
 CC IsoId=O15519-8; Sequence=VSP_000830;
 CC Name=9; Synonyms=Flame-1 beta;
 CC IsoId=O15519-9; Sequence=VSP_000830, VSP_000836, VSP_000837;
 CC Name=10; Synonyms=Flame-1 delta;
 CC IsoId=O15519-10; Sequence=VSP_000834, VSP_000835;
 CC Name=11; Synonyms=Usurpin beta;
 CC IsoId=O15519-11; Sequence=VSP_000838;
 CC Name=12; Synonyms=Usurpin gamma;
 CC IsoId=O15519-12; Sequence=VSP_000832, VSP_000833;
 CC Name=13;
 CC IsoId=O15519-13; Sequence=VSP_000831;
 CC Name=14;
 CC IsoId=O15519-14; Sequence=VSP_000839;
 CC -1- TISSUE SPECIFICITY: Widely expressed. Highest expression in
 CC skeletal muscle, pancreas, heart, kidney, placenta, and peripheral
 CC blood leukocytes. Also detected in diverse cell lines. Isoform 8
 CC is predominantly expressed in testis and skeletal muscle.
 CC -1- INDUCTION: Repressed by IL-2 after TCR stimulation, during
 CC progression to the S-phase of the cell cycle.
 CC -1- DOMAIN: The caspase domain lacks the active sites residues
 CC involved in catalysis.
 CC -1- PTM: Proteolytically processed; probably by caspase-8. Processing
 CC likely occurs at the DISC, generates subunit p43 and p12.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

Query Match 90.8%; Score 1635; DB 1; Length 480;
 Best Local Similarity 94.1%; Pred. No. 1e-114;
 Matches 319; Conservative 2; Mismatches 0; Indels 16; Gaps 1;

QY 1 MAEIGEDLDSDVSLIFLMKDMYMGKSKSKSPFLDLYVELEKNTLYAPDOLLLEKCL 60
 DB 97 MAEIGEDLDSDVSLIFLMKDMYMGKSKSKSPFLDLYVELEKNTLYAPDOLLLEKCL 156
 QY 61 KNHRIIDLKTKIKYKQSVQAGTSTRVYLOAIQKSLDPPNNRRLNKGSKKQRLKEQ 106
 DB 157 KNHRIIDLKTKIKYKQSVQAGTSTRVYLOAIQKSLDPPNNRRLNKGSKKQRLKEQ 216
 QY 107 ----EEPVKKSIOESBAFLPQSIPEERYKMKSPKGLICILIDCIGNETELLRLDTFTSLGY 162
 DB 217 LGAQOEPEVKKSIOESBAFLPQSIPEERYKMKSPKGLICILIDCIGNETELLRLDTFTSLGY 276
 QY 163 EVQKFLHLSHNGISQILGQAPCMPEHRDPSFCVCLVSRGSSQSVYGVDOQHSGJPLHNI 222
 DB 277 EVQKFLHLSHNGISQILGQAPCMPEHRDPSFCVCLVSRGSSQSVYGVDOQHSGJPLHNI 336
 QY 223 RRMFGDSCPYLAGKPMFPIQNYVVSDDQLBDSLLLEVDPAMNVKFAQKGLCTVH 282
 DB 337 RRMFGDSCPYLAGKPMFPIQNYVVSDDQLBDSLLLEVDPAMNVKFAQKGLCTVH 396
 QY 283 READPFWSLCTADMSLLFQSHSPSLYICLSQKLRQER 321
 DB 397 READPFWSLCTADMSLLFQSHSPSLYICLSQKLRQER 435

RESULT 2
 CELA_MOUSE STANDARD; PRT; 484 AA.

AC 035732; 035707; 035733;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CASP8 and PADD-like apoptosis regulator precursor (Cellular FLICE-like
 inhibitor protein) (c-FLIP) (Caspase-eight-related protein) (Casper)
 DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
 inducer of toxicity) (WRT) (Caspase homolog) (CASH) (Inhibitor of
 FLICE) (1-FLICE) (PADD-like antiapoptotic molecule 1) (Flame-1)
 DE (Ueaurin).
 DE CFLAR OR CASH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NX NCBI_TaxID=10090;
 RX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Liver;
 RX MEDLINE=97426025; PubMed=9289491;
 RA Golitsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianskii V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RT J. Biol. Chem. 272:19641-19644(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Heart;
 RX MEDLINE=97360133; PubMed=9217161;
 RA Immler W., Thome M., Hanne M., Schneider P., Hofmann K., Steiner V.,
 RA Boemer J.-L., Schroeber M., Burris K., Mattemann C., Rimoldi D.,
 RA French L.E., Schoppert J.;
 RT "Inhibition of death receptor signals by cellular FLIP.";
 RT Nature 388:190-195(1997).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20350661; PubMed=10894163;
 RA Yeh W.-C., Irie A., Elia A.J., Ng M., Shu H.-B., Wakeham A.,
 RA Mitsos C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.;
 RT "Requirement for Casper (c-FLIP) in regulation of death
 RT receptor-induced apoptosis and embryonic development.";
 RT Immunity 12:633-642(2000).

RN [4]
 RP FUNCTION.
 RX MEDLINE=20069388; PubMed=10602037;
 RA Wang J., Llobio A.A., Shen F., Hornung F., Minoto A., Ienardo M.J.;
 RT "Inhibition of Fas-mediated apoptosis by the B cell antigen receptor
 RT through c-FLIP.";
 RT Eur. J. Immunol. 30:155-163(2000).
 CC -1- FUNCTION: Apoptosis regulator protein which may function as a
 CC crucial link between cell survival and cell death pathways in
 CC mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
 CC apoptosis. A proteolytic fragment (p43) is likely retained in the
 CC death-inducing signaling complex (DISC) thereby blocking further
 CC recruitment and processing of caspase-8 at the complex. Full
 CC length and shorter isoforms have been shown either to induce
 CC (caspase) activity (By similarity).
 CC -1- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
 CC inducing signaling complex (DISC) formed by TNFRSF6, FADD and
 CC caspase-8. A proteolytic fragment (p43) stays associated with the
 CC DISC (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=FLIP-L, CASH alpha;
 CC IsoId=O35732-1; Sequence=Displayed;
 CC Name=2; Synonyms=FLIP-S, CASH beta;
 CC IsoId=O35732-2; Sequence=VSP_000842, VSP_000843;
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart.
 CC -1- DEVELOPMENTAL STAGE: At embryonic days E9.5 and E10.5 highest
 CC expression in developing heart.
 CC -1- INDUCTION: Isoform 1 but not isoform 2 is activated by BCR cross-
 CC linking in primary B-cells.
 CC -1- DOMAIN: The caspase domain lacks the active sites residues
 CC involved in catalysis.
 CC -1- PTM: Proteolytically processed, probably by caspase-8. Processing
 CC likely occurs at the DISC, generates subunit p43 and p12 (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; Y14041; CAA74368.1; -;
 DR EMBL; Y14042; CAA74369.1; -;
 DR EMBL; U97076; AAC53281.1; -;
 DR HSSP; O15806; 1QDU.
 DR MEROPS; C14.974; -;
 DR MGD; MGI1336166; CfIar.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICB_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR SMART; SM00031; DED; 2.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 KW Apoptosis; Repeat; Alternative splicing.
 FT CHAIN 1 380
 FT CHAIN 381 484
 FT CHAIN 485 484
 FT DOMAIN 6 78
 FT DOMAIN 97 175
 FT DOMAIN 268 363
 FT DOMAIN 421 425
 FT VARSPIC 208 218
 FT 21.


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FT  VARSLIC      219      480      /Ffid=VSP_000842.
FT  MISSING (In Isoform 2).
FT  CONFLICT     123      125      /Ffid=VSP_000843.
FT  MISSING (IN REF. 2).
SQ  SEQUENCE     484 AA, 55245 MW, 0BF7A92CB095F1F CRC64;

Query Match      55.9%; Score 1006.5; DB 1; Length 484;
Best Local Similarity 62.1%; Pred. No. 8.5e-68;
Matches 211; Conservative 41; Mismatches 67; Indels 21; Gaps 6;

QY  1 MAEIGEDLDKSPVSSFLF---MKDYGRGKISKSEKFLDLVVELEKLNVAAPDQDLLE 57
D  102 LMEIGESLDQNDVSSFLVTRITTDYGRGKIAKSKFLDLVLEKLNIAASDQDLLE 161
QY  56 KCLKNHRIIDELTKYIQYKQSGVQAGTGYRNVLAQAIQK-SLNDPS---NNFREBP---- 109
D  162 KCLKNHRIIDELTKYIQYKQSGVQAGTGYRNVLAQAIQK-SLNDPS---NNFREBP---- 220
QY  110 -----VKKSIOSEAFPLQSPIDPEERYKMKSPKIDICIIDICIGETELLADPTSTIG 161
D  221 YRDSQRTLVKTSIQSGAFPLPHIREETRYKQSKPDIICIIDICIGETELLADPTSTIG 280
QY  162 YEVOKFLHLSMHGISQILGQFACPMERHDYDSFVCVIVSRGSGSQSYGVQDTSGSLPHR 221
D  281 YHIQFLFPKSHDITQYRRAYSMAQODYDSFACVIVSLGSGSQSMWGRQVHSGFSLDH 340
QY  222 IRRMWDGSCPYLAGKPKMFTIONVYVSDGQLEDSSLLEVDPAMKNVEFKAKRGELCTV 281
D  341 YKMFPTGYTCPSLRKPKLPFIQNYVESIGSQLESQSS-LEVDGSPISKVDSKPLQPHRCTT 399
QY  282 HREADFPMWLCCTADWMLLEQSHSPSLYLQCLISQXKRCQR 321
D  400 HREADFPMWLCCTADWMLLEQSHSPSLYLQCLISQXKRCQR 439

DB  400 HREADFPMWLCCTADWMLLEQSHSPSLYLQCLISQXKRCQR 439

RESULT 3
ICB8 HUMAN      STANDARD;      PR1;      479 AA.
ID  ICB8 HUMAN      014676; 014791; 014792; 014793; 014795; 014796;
AC  014750; 014676; 014791; 014792; 014793; 014795; 014796;
AC  015780; 015805; Q8TD11; Q8TD12; Q8TD13; Q8TD14; Q8TD15; Q8TD15;
AC  Q9COK4; Q9COK8;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Caspase-8 precursor (BC 3.4.22.-) (ICE-1-like apoptotic protease 5)
DE  (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE  like protease) (FADD-1-like ICE) (FLICE) (Apoptotic cysteine protease)
DE  (Apoptotic protease Mch-5) (CAP4).
GN  CASP8 OR MCH5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_Taxid:9606;
RN  [1]
RN  SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3, 5, 6, 7 AND 8).
RP  TISSUE=B-cell, and Thymus;
RC  MEDLINE=96279827; PubMed=8681376;
RA  BOLDIN M.P., Goncharov T.M., Goltssev Y.V., Wallach D.;
RA  Bolin M.P., Goncharov T.M., Goltssev Y.V., Wallach D.;
RA  Kramer P.H., Peter M.E., Dixit V.M.;
RT  "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT  to the CD95 (Fas/Apo-1) death-inducing signaling complex.";
RL  Cell 85:817-827(1996).
RP  SEQUENCE FROM N.A. (ISOFORM 4).
RT  TISSUE=T-cell;

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RX  MEDLINE=96353838; PubMed=8755496;
RA  Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
RA  Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA  Litwack G., Alnemri E.S.;
RT  "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT  apoptotic cysteine protease containing two FADD-1-like domains.";
RT  Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RX  MEDLINE=99132295; PubMed=9931493;
RA  Grenier J., Teitz T., Wei T., Valentine V., Kidd V.J.;
RT  "Structure and chromosome localization of the human Casp8 gene.";
RL  Gene 226:225-232(1999).
RX  MEDLINE=97373543; PubMed=9228018;
RA  Srinivasula S.M., Ahmad M., O'Connell S., Bullrich F., Banks S.,
RA  Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA  Armstrong R.C., Alnemri E.S.;
RT  "FAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT  Fas/TNFR1-induced apoptosis.";
RL  J. Biol. Chem. 272:18542-18545(1997).
RX  MEDLINE=21100893; PubMed=11161814;
RA  Hadano S., Yanagisawa Y., Skaug J., Richter K., Nasir J.,
RA  Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA  Ikeda J.-E., Hayden M.R.;
RT  "Cloning and characterization of three novel genes, A152CR1, A152CR2,
RT  and A152CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT  critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL  Genomics 71:200-213(2001).
RX  MEDLINE=22005982; PubMed=12010809;
RA  Himeji D., Horikuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA  Harada M.;
RT  "Characterization of caspase-8L, a novel isoform of caspase-8 that
RT  behaves as an inhibitor of the caspase cascade.";
RL  Blood 99:4070-4078(2002).
RX  MEDLINE=21927603; PubMed=11917123;
RA  Breckenridge D.G., Nguyen M., Kuppig S., Reith M., Shore G.C.;
RT  "The procaspase-8 isoform, procaspase-8L, recruited to the BAP1
RT  complex at the endoplasmic reticulum.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
RX  MEDLINE=22388257; PubMed=12477932;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RA  Brownstein M.J., Udaif T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Huliy K.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzyzinski M.I., Skalska M., Marra M.A.,
RA  Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT  "Generation and mouse cDNA analysis of more than 15,000 full-length
RT  human and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN [10]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=97121412; PubMed=8962078;
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
 Alnemri E.S.;
 RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/ABO-1
 protease Mcs5 is a CrmA-inhibitable protease that activates multiple
 Ced-3/ICE-like cysteine proteases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
 RN [11]
 RP FUNCTION.
 RX MEDLINE=97160607; PubMed=9006941;
 RA Muzio M., Salvesen G.S., Dixit V.M.;
 RT "Flice induced apoptosis in a cell-free system. Cleavage of caspase
 zymogens.";
 RL J. Biol. Chem. 272:2952-2956(1997).
 RN [12]
 RP PROCESSING.
 RX MEDLINE=9737557; PubMed=9184224;
 RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
 Kramer P.H., Peter M.E.;
 RT "Flice is activated by association with the CD95 death-inducing
 signaling complex (DISC).";
 RL EMBO J. 16:2794-2804(1997).
 RN [13]
 RP CHARACTERIZATION OF ISOFORM 7.
 RX MEDLINE=20318377; PubMed=10360845;
 RA Horinchi T., Hameji D., Tsukamoto H., Harashima S., Hashimura C.,
 Hayashi K.;
 RT "Dominant expression of a novel splice variant of caspase-8 in human
 peripheral blood lymphocytes.";
 RL Biochem. Biophys. Res. Commun. 272:877-881(2000).
 RN [14]
 RP INTERACTION WITH BCL2, BCL2L1 AND BCLP31.
 RX MEDLINE=97477382; PubMed=9334338;
 RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
 Cromlish J.A., Shore G.C.;
 RT "B28 Bap1, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
 endoplasmic reticulum.";
 RL J. Cell Biol. 139:327-338(1997).
 RN [15]
 RP INTERACTION WITH PEAL5.
 RX MEDLINE=99369240; PubMed=10442611;
 RA Condorelli G., Vigiotti G., Cafieri A., Trecia A., Andalo P.,
 Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
 RT "PEB/BEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
 induced apoptosis.";
 RL Oncogene 18:4409-4415(1999).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=99451259; PubMed=10508784;
 RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
 Wu J.C., Tomaselli K.J., Gruetter M.G.;
 RT "The three-dimensional structure of caspase-8: an initiator enzyme in
 apoptosis.";
 RL Structure 7:1125-1133(1999).
 RN [17]
 RP VARIANT CASP8D TRP-248.
 RX MEDLINE=2239940; PubMed=12353035;
 RA Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
 Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
 Akinson T.P., Straus S.E., Lemaire M.J.;
 RT "Phenotypic defects in lymphocyte activation caused by caspase-8
 mutations lead to human immunodeficiency.";
 RL Nature 419:395-399(2002).
 RN [18]
 RP FUNCTION: Most upstream protease of the activation cascade of
 caspases responsible for the TNFRSF6/Fas mediated and TNFRS1A
 induced cell death. Binding to the adapter molecule FADD recruits
 it to either receptor. The resulting aggregate called death-
 inducing signaling complex (DISC) performs Casp8 proteolytic
 activation. The active dimeric enzyme is then liberated from the
 DISC and free to activate downstream apoptotic proteases.
 CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,

CC CAP3 and CAP6) are likely retained in the DISC. Cleaves and
 CC activates Casp3, Casp4, Casp6, Casp7, Casp9 and Casp10. May
 CC participate in the G2M apoptotic pathways. Cleaves ADPRT.
 CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
 CC Likely target for the complex virus CRMA death inhibitory protein.
 CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
 CC with the pro-apoptotic activity of the complex.
 CC SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
 CC Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
 CC endoplasmic reticulum with a complex containing BCLP31, BAP29,
 CC BCL2 and/or BCL2L1.
 CC CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=9;
 CC Name=1; Synonyms=Alpha-1;
 CC IsoId=Q14790-1; Sequence=Displayed;
 CC Name=2; Synonyms=Alpha-2, MCH5-beta;
 CC IsoId=Q14790-2; Sequence=VSP_000810;
 CC
 Query Match 17.4%; Score 313; DB 1; Length 479;
 Best Local Similarity 26.8%; Pred. No. Se-16;
 Matches 95; Conservative 75; Mismatches 117; Indels 68; Gaps 14;
 QY 3 EIGEDLDKSDVSLFLMKDYVGRGKISKRSFLDLYVELEKLVLPDQDLLEKICLN 62
 DB 107 QSEVSRSELSFFFLQGEISKCKLDDNNLDFIEMKRVILGEGKDLKRVCAQ 166
 QY 63 IHRIDKTKIQKYKQ-----SVQAGSTRNVLOAIIQSLSDPSNNFPEPKYSIQ 115
 DB 167 IKSLIKTI-INYEERFSKRSSESSLEGSPEFSNGEELGVWITDSP---RE-----Q 215
 QY 116 ESEAFLOPSIPERKPKMSKPLGICLIIDCIG-----NETEL-----LR 154
 DB 216 DSES---QTL-DKYQMSKSPRGYCLIIINNPFKARKRVKLSIRNRNTHLDAGLT 271
 QY 155 DFTSLGVQKFLHSMGSIQIGQACPEHEHDYSPVCLVSRGSGSVYGVDT 214
 DB 272 TFEELHFEIKFHDCTQVQIYEIKIYQLM-DHNMDCFLICILSHDKGIIVGTQGE 330
 QY 215 SGPLPHIRFMFMGSPCYLACKPKMFIC-----NY---VVSQQLDSSLLFPD--GP 264
 DB 331 A-FLTELTSQFTGKCSLAKSPKVFPIQACQGDNYKGIPEVDSSEQYLENDLSSP 388
 QY 265 AMKNVEFKAKRGKGLCTVHREDFWMLCTADMSLLEQSSSPSYLQCLSQKLRQ 319
 DB 389 QRIYIP-----DEADFLGMATVNNCVSYRNAPAGTWYIQSLCQSLAE 431
 RESULT 4
 ICE8 MOUSE STANDARD; PRT; 480 AA.
 ID ICE8 MOUSE
 AC 089110; O35669;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-).
 GN CASP8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=129/SvJ;
 RX MEDLINE=98316661; PubMed=9654089;
 RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
 RT "Molecular cloning and characterization of mouse caspase-8.";
 RL Eur. J. Biochem. 253:399-405(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=99057979; PubMed=9837723;
 RA Van de Craen M., Van Loo G., Declercq W., Schotte P.,
 van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,

RA Vandenberg P.;
RT "Molecular cloning and identification of murine caspase-8";
RL J. Mol. Biol. 284:1017-1026(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantucci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulady S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 57-476 FROM N.A.
RA Kioschis P., Kischkel F., Pousotka A., Kramer P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs Casp8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates Casp3, Casp4, Casp6, Casp7, Casp9 and Casp10. May
CC participate in the G2M apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC Likely target for the cowpox virus CRMA death inhibitory protein.
CC -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
CC -!- INTERACTS WITH FADD, cIcar and Peals (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
CC Highest expression in spleen, thymus, lung, liver and kidney.
CC Lower expression in heart, brain, testis and skeletal muscle.
CC -!- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
CC day 7.
CC -!- PTM: Generation of the subunits requires association with the
CC death-inducing signaling complex (DISC), whereas additional
CC processing is likely due to the autocatalytic activity of the
CC activated protease. G2MB and Casp10 can be involved in these
CC processing events (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 2 death effector (DEE) domains.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF067841; AAC40132.1; -
DR EMBL; AF067835; AAC40132.1; JOINED.
DR EMBL; AF067836; AAC40132.1; JOINED.
DR EMBL; AF067837; AAC40132.1; JOINED.
DR EMBL; AF067838; AAC40132.1; JOINED.

DR EMBL; AF067839; AAC40132.1; JOINED.
DR EMBL; AF067840; AAC40132.1; JOINED.
DR EMBL; AF067843; AAC40131.1; -
DR EMBL; AJ007749; CA07677.1; -
DR EMBL; BC006737; AAH06737.1; -
DR EMBL; BC049955; AAH49955.1; -
DR EMBL; AJ000641; CA004196.1; -
DR HSPB; Q15806; ICDU.
DR MEROPS; C14.009; -
DR MG; MG1:1261423; Casp8.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005634; Cnucleus; IDA.
DR GO; GO:0004205; F:caspase-8 activity; IDA.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR SMART; SK00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
KW Hydroxylase, Thiol protease, Apoptosis, Zymogen, Repeat.
FT PROPEP 1 218
FT CHAIN 1 219
FT PROPEP 219 376
FT CHAIN 377 387
FT CHAIN 388 480
FT ACT_SITE 319 319
FT ACT_SITE 362 362
FT DOMAIN 3 80
FT DOMAIN 101 177
FT CONFLICT 68 71
FT CONFLICT 94 99
FT CONFLICT 96 96
FT CONFLICT 103 107
FT CONFLICT 475 475
SQ
Query Match 480 AA; 55356 MW; 045268E3D5ED4F CRC64;
Best Local Similarity 26.5%; Score 297; DB 1; Length 480;
Matches 95; Conservative 70; Mismatches 120; Indels 74; Gaps 14;
OY 3 EIGEDDDKSVSLIIMADVWGROKISKSEKSFLLVLELEKTLNVAPDQDLLEKCLKN 62
DB 107 KISEEVESELEKRFKFLNNELPKCELDJLSLIFEMERGTWLANLETLISICDQ 166
OY 63 IHRIDIKTKIOKY-----KQVOGAGTSYRVNLOAAIOLSLK--DPSNNFREPYKKS 113
DB 167 VNK-SLLGKIEDYERSTERMSLGRBELPESVLD---EMSLKXAEICDSPRE----- 216
OY 114 IOSESEFLPOSIDPEERYKKKSRPLGICLI-----DCIGNE 149
DB 217 -QSEBSRTSDKV---YQKNKPRGVCILINNHSFKAREDTQLRKXKDKGTDC--D 268
OY 150 TELLRFTSLGVEOKFHLNMGHISGLIGFACMPHPRDYSPVCLVSRGSGSQSYG 209
DB 269 KEMLSKTFKELNHEIYSYDCTANHEHLEBYQ-SADHKKDCICILSHGDKGVYGG 327
OY 210 VPDTHGSLPLHITRRFMWDCSPYLAQKPYFFI0-----NVV--VSD--GQLEDSLSLE 260
DB 328 TDSEKES--IYDLSYFTSGSKPSPSLGKXKIFFIOACGGSNFQKGVPEADPEEQNMHLE 385
OY 261 VDPGPAKNVVEFKAKGGLCTVAREADFFWSLCTAAMSLLEGSHSSPSLYLCLCSQKLRQ 319
DB 386 VDSSSHKXV-----IPDEADFLGMAITVKNCSYNDPVPNGVTYISLQSLRE 433

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RESULT 5
ICEA_HUMAN STANDARD; PRT; 521 AA.
ID AC Q92851; Q8WY08; Q93845; Q9Y2U6; Q9Y2U7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-10 precursor (EC 3.4.22.-) (ICE-1-like apoptotic protease 4)
DE (Apoptosis protease Mch-4) (PAS-associated death domain protein
DE Interleukin-1b-converting enzyme 2) (FICE2).
DE CASP10 OR MCH4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=T-cell;
RX MEDLINE=9635383; PubMed=8755496;
RX Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RX Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.G.,
RX Litwack G., Alnemri E.S.;
RX "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RX apoptotic cysteine protease containing two FADD-like domains.";
RX Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=9719783; PubMed=9045686;
RX Vincenz C., Dixit V.M.;
RX "Fas-associated death domain protein interleukin-beta-converting
RX enzyme 2 (FICE2), an ICE/Ced-3 homologue, is proximally involved in
RX CD95- and p55-mediated death signaling.";
RX J. Biol. Chem. 272:6578-6583(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT ILE-410.
RC TISSUE=Spleen, and Thymus;
RX MEDLINE=9921459; PubMed=10187817;
RX Ng P.W., Porter A.G., Janicke R.U.;
RX "Molecular cloning and characterization of two novel pro-apoptotic
RX isoforms of caspase-10.";
RX J. Biol. Chem. 274:10301-10308(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=2110089; PubMed=11161814;
RX Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RX Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RX Ikeda J.-E., Hayden M.R.;
RX "Cloning and characterization of three novel genes, AHS2CR1, AHS2CR2,
RX and AHS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RX critical region at chromosome 2q33-q34; candidate genes for ALS2.";
RX Genomics 71:200-213(2001).
RN [5]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=9712141; PubMed=8962078;
RX Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RX Alnemri E.S.;
RX "Molecular ordering of the Fas-apoptotic pathway: the Fas/Apo-1
RX protease Mch3 is a CrmA-inhibitable protease that activates multiple
RX Ced-3/ICE-like cysteine proteases.";
RX Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
RN [6]
RP VARIANT ALPS2 PHE-285, AND VARIANT ILE-410.
RX MEDLINE=9933325; PubMed=10412980;
RX Wang J., Zheng L., Lobito A., Chan F.K., Dale J., Sneller M., Yao X.,
RX Puck J.M., Straus S.E., Lenardo M.J.;
RX "Inherited human caspase 10 mutations underlie defective lymphocyte
RX and dendritic cell apoptosis in autoimmune lymphoproliferative
RX syndrome type II";
RX Cell 98:47-58(1999).
RN [7]
RP FUNCTION: Involved in the activation cascade of caspases
RN responsible for apoptosis execution. Recruited to both Fas- and
RN TNFR-1 receptors in a FADD dependent manner. May participate in
RN the granzyme B apoptotic pathways. Cleaves and activates caspase-

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CC 3, -4, -6, -7, -8, and -9. Hydrolyzes the small-molecule
CC substrates, Tyr-Val-Ala-Asp-|-AMC and Asp-Glu-Val-Asp-|-AMC.
CC -1- FUNCTION: Isoform C is proteolytically inactive.
CC -1- SUBUNIT: Heterodimer of a 23/17 kDa (p23/17) depending on the
CC splicing events and a 12 kDa (p12) subunit.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=A; Synonyms=10-A;
CC IsoId=Q92851-1; Sequence=Displayed;
CC Name=B; Synonyms=10-B;
CC IsoId=Q92851-2; Sequence=VSP_000819, VSP_000820;
CC Name=C; Synonyms=10-C;
CC IsoId=Q92851-3; Sequence=VSP_000821, VSP_000822;
CC -1- TISSUE SPECIFICITY: Detectable in most tissues. Lowest expression
CC is seen in brain, kidney, prostate, testis and colon.
CC -1- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE
CC THE TWO ACTIVE SUBUNITS.
CC -1- DISEASE: Defects in CASP10 are the cause of type II autoimmune
CC lymphoproliferative syndrome (ALPS2) [MIM:603909]. ALPS2 is
CC characterized by abnormal lymphocyte and dendritic cell
CC homeostasis and immune regulatory defects.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
CC -----
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CC -----
DR EMBL; U60519; AAC5064.1; -
DR EMBL; U86214; AAB46730.1; -
DR EMBL; AF111344; AAD28402.1; -
DR EMBL; AF111345; AAD28403.1; -
DR EMBL; AB038978; BAB32553.1; -
DR EMBL; AB038973; BAB32553.1; JOINED.
DR EMBL; AB038974; BAB32553.1; JOINED.
DR EMBL; AB038975; BAB32553.1; JOINED.
DR EMBL; AB038977; BAB32553.1; JOINED.
DR EMBL; AB038979; BAB32554.1; -
DR EMBL; AB038973; BAB32554.1; JOINED.
DR EMBL; AB038974; BAB32554.1; JOINED.
DR EMBL; AB038975; BAB32554.1; JOINED.
DR EMBL; AB038976; BAB32554.1; JOINED.
DR EMBL; AB038977; BAB32554.1; JOINED.
DR HSPB; Q15806; IQDU.
DR MEROPS; C14.011; -
DR Genew; HGNC:1500; CASP10.
DR MIM; 601762; -
DR MIM; 603909; -
DR GO; GO:0004199; F:caspase activity; TAS.
DR GO; GO:0004206; F:caspase-10 activity; TAS.
DR GO; GO:0006517; P:induction of apoptosis; TAS.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2
DR Pfam; PR00656; Peptidase_C14; 1
DR PRINTS; PR00376; ILIBENZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
DR Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat;
DR Alternative splicing; Polymorphism; Disease mutation.
FT PROPEP 1 219
FT CHAIN 220 415 CASPASE-10 SUBUNIT P23/17.

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FT CHAIN 416 521 CASPASE-10 SUBUNIT P12.
FT DOMAIN 19 97 DED 1.
FT DOMAIN 114 187 DED 2.
FT ACT_SITE 358 358 BY SIMILARITY.
FT ACT_SITE 401 401 BY SIMILARITY.
FT VARSPIC 229 271 Missing (in isoform B).
FT VARSPIC 473 521 /Ftid=VSP_000819.
FT VARSPIC 521 521 MLKPLKMTKMTKGRKTRVWGAKOISATSLPTAISAQTRPP
FT VARSPIC 521 521 MRKMSVS -> HEDILSITLVANDVSRVDSKQTKQMP
FT VARSPIC 521 521 OPAFLTKKLVFPVPLDALSI (in isoform B).
FT VARSPIC 521 521 /Ftid=VSP_000820.
FT VARSPIC 241 273 GNRATNCRAPLVSCMGAGASANTINSTRKRA -> EGSC
FT VARSPIC 241 273 VDSSEFQRPFLCHQDPQLVLPBQRTNRP (in isoform
FT VARSPIC 241 273 C).
FT VARSPIC 274 521 /Ftid=VSP_000821.
FT VARSPIC 274 521 Missing (in isoform C).
FT VARSPIC 285 285 /Ftid=VSP_000822.
FT VARSPIC 285 285 L -> F (in ALPS2).
FT VARSPIC 410 410 /Ftid=VAR_014071.
FT VARSPIC 410 410 V -> I.
FT CONFLICT 68 68 E -> G (IN REF. 2).
FT CONFLICT 268 268 T -> A (IN REF. 3).
SQ SEQUENCE 521 AA; 58950 MW; 840348AE6028243 CRC64;

Query Match 13.8%; Score 248.5; DB 1; Length 521;
Best Local Similarity 25.3%; Pred. No. 3.7e-11;
Matches 91; Conservative 60; Mismatches 154; Indels 55; Gaps 11;

QY 3 EIGEDLDSDVSLFLMKDYMGKGRKISKEKSFIDLVELEKINLVAPQDLLE----- 57
DB 121 ELSEIDSEIDENLKMIFLKDSLPR-----TENTSLSTFLAFLEKKGKIDEDVLTLDELCKMT 176
QY 58 ---KCLKNIRIDLTXTIQ-----KYKOSVQC-----AGTSYRVNLQAIKSLKDP- 101
DB 177 VVPLKLRRIEKKYKKEKAQIYTPPVDEAESEYQGEELVQOTVTKFLEALPEBSQWNGH 236
QY 102 -----SNNPREBPKVKSIOSEAFIPQSIPEER-----TKMSKPLGICLII----- 143
DB 237 AGSNANRATNGAPSLVSRGMOGASANTINSETSKRAAVYRRNRRHGLCVIYNHSPTS 296
QY 144 --DCTG--NETELLRDFTSLGKYVQKFLHLSMHGISQLIGOPACVPERHDYDSFYCVLV 199
DB 297 LKDRQGTAKDAEILSHVQWLGFTVHINNVYTKYEMEMVLOKCKNPAHADGCFEFCIL 356
QY 200 SSGSGSOSVGVDOHTSGSLPLHIRMFMGDSCPYLAKRKPFIQNVVSDGLEDSLL 259
DB 357 THGRGAVYSDE--ALTFIREINSHFTALQCPFLAKPKLFIQ--ACQGEIOPSvsi 412
QY 260 EVDGPMKNVFEKQKRGRLCTVREADFWSLCTADMSLLQSHSSPSLYLQCLSQKLRQ 319
DB 413 EADALNPQAPTSIQD-----SIPADADFLGLATVPYVSFRVVEGSSWYIQGLCNHLKX 468

RESULT 6
ICE6_HUMAN STANDARD; PRT; 293 AA.
AC P55212; O9BOE7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN Casp6 OR MCH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=95316841; PubMed=7796396;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene

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RT family.";
RL Cancer Res. 55:2737-2742(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-M.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Wittek L.A., Nickerson D.A.;
RN Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udell T.B., Toshynki S., Carninci P., Mullany S.J.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schneringer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [4]
RP PROCESSING.
RC TISSUE=Lymphocytes;
RX MEDLINE=97059171; PubMed=8900201;
RA Striniवासula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
RT mediator CPP32.";
RL J. Biol. Chem. 271:27099-27106(1996).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death.
CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=Alpha;
CC IsoId=P55212-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P55212-2; Sequence=VSP_000805;
CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS.
CC -1- SIMILARITY: Belongs to peptidase family C14.
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CC -----
DR EMBL; U20536; AAC50168.1; -
DR EMBL; U20537; AAC50169.1; -
DR EMBL; AY254046; AA063494.1; -
DR EMBL; BC000305; AA00305.1; -
DR EMBL; BC004460; AA004460.1; -
DR HSSP; P42574; 1PAU.

```

Query	Subject	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	111 KKSIOSEAFLEPQSI--PEERKMKSKPLGICLID	11.1%;	Score 199;	DB 1;	Length 293;			
QY	16 EENMTITDPAFYKEMDPKAKYKMRRRGILFLNHRFPFWHLTLPRRGTCADRDN--	Best Local Similarity 27.5%;	Pred. No. 8.8e-08;					
Db	74 LTRRFSDLGFEVYKCFNDLKAEEILLKIHVSIV	Matches 69;	Conservative 33;	Mismatches 75;	Indels 74;	Gaps 10		
QY	153 LRDFTFSLGYEYOKF-----LHDSMEGISQLGQFACMEHRHDYDSFVCYLVSRSQSG							
Db	126 HIAYAKIEIQTTLTGL-----FKDKDKCHSLGKKEKIFILACRGNQHDVPIPLDV							
QY	249 SDGQLS--DSSLLEVGPAMKQVEFKQKRGICVYHRADFFWISLCTADMSLLEQSHSP							
Db	178 VDNQTKLDTNITEVDAA-----YTLTPAADLPMCTSYAEIGVSHRETVNG							
QY	206 SYVGVV-----QTHSGPLHRIHRFMQDSCPYLAGKRMFFIC-----NYTV							
Db	126 HIAYAKIEIQTTLTGL-----FKDKDKCHSLGKKEKIFILACRGNQHDVPIPLDV							
QY	307 SLYLQGLSQKL 317							
Db	226 SWYIDLCCEML 236							
RESULT 7								
ICB2_CHICK								
ID_ICB2_CHICK	STANDARD;	PRT;	424 AA.					
AC	Q98943;							
DT	01-NOV-1997 (Rel. 35, Created)							
DT	01-NOV-1997 (Rel. 35, Last sequence update)							
DT	10-OCT-2003 (Rel. 42, Last annotation update)							
DE	Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-11/1S).							
GN	CASP2 OR ICH1.							
OS	Gallus gallus (Chicken).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;							
OC	Gallus.							
NC	NCBI_TaxID=9031;							
NP	(1)							
SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).								

[illegible]

QY 61 KNIRHIDKTKIQKYKQVQAGATSYRNLQAAIQKSLKDPSSNNFREPEVYKSGIOSEAF 120
 Db 82 QETKQOHLAEMILKTNESLFRGIATLEQRYGNSNPLPLSSSCNSKRPRLIVESHLSGDG 141
 QY 121 LFOSTPEER-----YKMSKPLDGLI-----IDCIG 147
 Db 142 PP--TTPVGHCTPEFYRDHQLAKKLISEPRGLALISNHFSEKOLEYRSGGDVCA- 198
 QY 148 NTELLRDFTSLGYEVQKFLISMHGISQILGQFACMPREHRYDSFVCVLVRGSGSQV 207
 Db 199 -SLELL-----FKHLGQVIVFHHQSAEHESSALHFSTKLPHQDVDSCTIVALLSHGVEGV 254
 QY 208 YVVDQTHSGLPNHRNFMGDSCPYLAGKPKFFIO-----NTVSDQLEDSS- 257
 Db 255 YGTD--GKLLQLOEAFRLFDNANCPNQNKPFFIOACRGDETRGVDQDRDKERSDSP 312
 QY 258 -LLEYDGPAMKRVETKQKRG--LC-----TVHEADPFMSICTADMSLLEGS 302
 Db 313 GGEESDANKENTKRLRLEPRSDMTCGACLKGTAAKNTKRGSYTALTTVAEDSRDT 372
 QY 303 HSSPSLYLQCLSQKLRQERGTIPSGGTTESKDM 335
 Db 373 HVADMVLK--VVRQIKQREGYAPGTEFHRCKEM 403

RESULT 8
 ICE3_MOUSE STANDARD; PRT; 277 AA.
 AC P70677; O08668; Q9QW14;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (Bg 3.4.22.) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1) (SCA-1) (LICE).
 GN CASP3 OR CPP32.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNeice I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme and CED-3.";
 RL Oncogene 13:749-755(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced by a withdrawal of NGF.";
 RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361; Declercq W., van den Brande I., van de Craen W., Vandenaebelle P., Schotte P., van Cleefinge W., Beyaert R., Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hochstim R.F., Jordan H., Moore T., Wax S.I., Wang G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Wuzny D.W., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O., Fortin J.-P., Sekaly R.-P.;
 RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PAR) at a 216-Asp-1-Gly-217 bond. Cleaves and activatessterol regulatory element binding proteins (SREBPs) between the basic helix-loop-helix leucine zipper domain and the membrane attachment domain. Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 Kda (p17) and a 12 Kda (p12) subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain, skeletal muscle and kidney.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain, skeletal muscle and kidney.
 CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROPEPTASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROPEPTASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
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 CC EMBL: U54803; AAC52768.1; -.
 CC EMBL: U54802; AAC52768.1; JOINED.
 CC EMBL: U49929; AAC52764.1; -.
 CC EMBL: D86352; BAA21727.1; -.
 CC EMBL: Y13086; CAA73528.1; -.
 CC EMBL: U19522; AAC53196.1; -.
 CC EMBL: BC038825; AAH38825.2; -.
 CC EMBL: U63720; AAD09504.1; -.
 CC PIR: JCS410; JCS410.
 CC HSSP: P42574; LPAU.
 CC MEROPS: C14.003; -.
 CC MGDI: MGDI:107739; Casp3.
 CC InterPro: IPR002138; ICE_p10.
 CC InterPro: IPR001309; ICE_p20.

DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; ILIBENZYME.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 RU PROPEP 1 9
 FT PROPEP 10 28 BY SIMILARITY.
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT CONFLICT 17 17 E -> G (IN REF. 2).
 FT CONFLICT 51 51 N -> T (IN REF. 2).
 FT CONFLICT 63 65 SRS -> ARN (IN REF. 6).
 FT CONFLICT 84 84 Q -> E (IN REF. 2).
 FT CONFLICT 95 95 D -> E (IN REF. 2).
 FT CONFLICT 97 97 L -> M (IN REF. 2).
 FT CONFLICT 128 128 Y -> F (IN REF. 2).
 FT CONFLICT 135 135 E -> D (IN REF. 2).
 FT CONFLICT 231 231 E -> Q (IN REF. 6).
 FT CONFLICT 262 262 I -> F (IN REF. 6).
 SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;
 Query Match 10.5%; Score 188.5; DB 1; Length 277;
 Best Local Similarity 28.9%; Pred. No. 5e-07; 92; Indels 37; Gaps 11;
 Matches 67; Conservative 36; Mismatches 3;
 QY 103 NNPREEPV--KKSIOSEAEFLPOSIEERYKMKSKPLGICLIID-----CTGN 148
 DB 14 NNFVKTTHSKSV--DSGIYLDSS-----YKMDYPMGICIIINNNKFKSTGMSRSRG 67
 QY 149 ETEL--LRDTFTSLGVEVQKFLHSMHGSLQILGACACPERHVDSPFCVLSKGSQS 206
 DB 68 DVAAANRETFMGKTKQVRKNDLREDLIELMDVS--KEDSKSSPFVCVILSHDGEV 126
 QY 207 VVGADQTHSLPLPHIRMFMDSCPYLAGKPMKPFICQNVVSDQLEDSLLEVDCGPM 266
 DB 127 IYGV---INGVELKSLTSPFGDYCRSLNKPFLFIQ---ACRGTEIDCG--IETDSGT- 178
 QY 267 KNVFKAKQKGLCTVHEADFMSLCTADMSLIEGSHSSPSLYLQCLSKLR 318
 DB 179 -DERMACQK-----IPEADFLVAYSTADGYVWRNSKGSWFIQSLCSMLK 224
 RESULT 9
 ICE3_RAT STANDARD; PRT; 277 AA.
 AC P55213; P70543; P97699; G62993;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 protease) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 CS CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., Moniece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 a cysteine protease resembling interleukin-1 beta converting enzyme
 and CED-3.";
 RL Oncogene 13:749-755(1996).
 RN [2]

RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Tidovich A.M., Desanti A., Tilly K.I.,
 RA Hirschfield A.N., Tilly J.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
 RT endonuclease activity from morphological apoptosis in granulosa cells
 of the ovarian follicle.";
 RL Endocrinology 136:5042-5053(1995).
 RU [3]
 SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184204; PubMed=9030616;
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
 RA Rostock P., Jr., Poirier G.G., Paul S.M.;
 RT "Cloning and expression of a rat brain interleukin-1beta-converting
 RT enzyme (ICE)-related protease (IRP) and its possible role in
 RT apoptosis of cultured cerebellar granule neurons.";
 RL J. Neurosci. 17:1561-1569(1997).
 [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RU Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-ASP--GLY-217 bond. Cleaves and activates steroid regulatory
 CC element binding proteins (SRBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC cleaves and activates caspase-6, -7 and -9 (by similarity).
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
 CC BUT NOT IN KIDNEY OR TESTIS.
 CC -1- DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions
 CC of the developing brain, but down-regulated to low levels in the
 CC adult brain.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC -----
 DR EMBL: U49930; AAC52765.1; -
 DR EMBL: U34685; AAC52261.1; -
 DR EMBL: U84410; AAB41792.1; -
 DR EMBL: U58656; AAB02722.1; -
 DR PIR: I67437; I67437.
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.003; -
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; ILIBENZYME.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.


```

FT PROPEP 1 9 BY SIMILARITY.
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT CONFLICT 25 29 KMSDS -> QVD (IN REF. 4).
FT CONFLICT 170 170 C -> S (IN REF. 2).
FT CONFLICT 178 178 T -> A (IN REF. 2).
FT CONFLICT 182 182 M -> V (IN REF. 2).
FT CONFLICT 187 187 I -> K (IN REF. 2).
FT CONFLICT 190 190 E -> G (IN REF. 2).
FT CONFLICT 199 199 T -> S (IN REF. 3).
FT CONFLICT 211 211 D -> G (IN REF. 2).
FT CONFLICT 236 236 L -> I (IN REF. 4).
FT CONFLICT 245 245 T -> M (IN REF. 3).
SQ SEQUENCE 277 AA; 31491 MW; ADABP418E2507402 CRC64;

Query Match 10.3%; Score 185.5; DB 1; Length 277;
Best Local Similarity 27.5%; Pred. No. 8.36-07;
Matches 64; Conservative 37; Mismatches 93; Indels 39; Gaps 8;

QY 103 NNFRPEPVKKS-IGESSEFLPQSIPEERYKKKSPGLGICLIID-----CIGNETEL 151
D 14 NNFRKTHGSKMSDGIYLDSS-----YKRDYPEWGLCIIINNNKPHKSTGMSANRGTD 68
QY 152 L-----LRDFTSLGYEVQKFLHLSMHGICQLGQFACMPHRDYDSFVCVLYSRGSGQGV 207
D 69 VDAANLRTEFWALKREYVANKNDLIREIMELMDSVS-KEDHSKRSSFVCVILSHGEQV 127
QY 208 YGVDTHTGCLPLHNRFRFMQDSCPYLAGKPKFFIQ--NYVVSQGLEDSLLLEVQGA 265
D 128 FG---TNGPVDLKLITSEFRGDYCRSLTGKPKFLIIQACRGTELDGIEFDSTGDDMAC 184
QY 266 MGNVFEKAKQKRGKGLCTVREADFWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 318
D 165 QK-----IPVADFVLYAVSTAFQYVSRMSRSGSWFIQSLCMKX 224

RESULT 10
ICB3_XENLA STANDARD; PRT; 282 AA.
AC P55866;
ID 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3)
DE (CASP-3) (XCP32).
GN XENOPUS laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184166; PubMed=9030578;
RA Yaeita Y., Nakajima K.,
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
RT myoblastic cell line derived from tadpole tail."
RT J. Biol. Chem. 272:5122-5127(1997).
CC -I- FUNCTION: Important mediator of apoptosis. At the onset of
CC apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase
CC (PARP) at a 216-ASP-Gly-217 bond (By similarity).
CC -I- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12)
CC subunits.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- MISCELLANEOUS: The subunits are derived from the precursor
CC sequence by a probable autocatalytic mechanism and probably by
CC other caspases (By similarity).
CC -I- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL: D89784; BAAL4018.1; -.
DR HSBP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBENZYM2.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 2
FT CHAIN 187 282 APOPAIN P17 SUBUNIT.
FT ACT_SITE 131 131 BY SIMILARITY.
FT ACT_SITE 174 174 BY SIMILARITY.
SQ SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;

Query Match 10.3%; Score 185.5; DB 1; Length 282;
Best Local Similarity 29.4%; Pred. No. 8.5e-07;
Matches 63; Conservative 33; Mismatches 71; Indels 47; Gaps 11;

QY 126 ERYKMSKPKGICLIID-----CIGNETEL-----LRDFTSLGYEV-----QKELH 169
D 46 QNRTYVPEWGLCIIINNNKPHSSNMAVANGTDVALKLHETFTGLGYEVAVCNDQK--- 102
QY 170 LSHMGISQLIGQACNPF--HRDYSPVCVLYSRGSGQ-SYGVQDHTGSLPLH--HIRR 224
D 103 -----SSDITGLRLKLTSEEDHSKRSSFVCVILSHGEDSGICGV-----VPIHKNTLD 152
QY 225 MFGDSCPYLAGKPKFFIQNYVVSQGLEDSLLLEVQPAKQVFEKAKRGKGLCTVARE 284
D 153 LFRGDKTKLVGKPKFFIQ---ACKGTLDSC-IETSCSPRRRIQ-----RIQVE 201
QY 285 ADFWWSLCTADMSLLEQSHSSPSLYLQCLSQKLR 318
D 202 ADFVLYAVSTVPGYCSWRMDGMSWFIQSLCMKX 235

RESULT 11
ICB3_CRILIO STANDARD; PRT; 277 AA.
ID ICB3_CRILIO
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPR-32) (Caspase-3) (CASP-3) (SRBP cleavage activity 1)
DE (SCA-1).
GN CRICETULUS longicaudatus (Long-tailed hamster) (Chinese hamster).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=9618185; PubMed=8605870;
RA Wang X., Zielinski N.G., Yang J., Sakai J., Brown M.S.,
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis."

```


RL EMBL J. 15:1012-1020(1996).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-1-gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 (PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC
 CC EMBL, U27463; AAB01511.1; -.
 CC HSBP, P42574; 1PAU.
 CC MEROPS, C14.003; -.
 CC InterPro: IPR002138; ICE_P10.
 CC InterPro: IPR001309; ICE_P20.
 CC InterPro: IPR002398; Peptidase C14.
 CC Pfam: PF00656; Peptidase C14; I.
 CC PRINTS, PR00376; IILBGNZME.
 CC SMART, SMO0115; CASC; 1.
 CC PROSITE, PS01122; CASPASE_CYS; 1.
 CC PROSITE, PS01121; CASPASE_HIS; 1.
 CC PROSITE, PS50207; CASPASE_P10; 1.
 CC PROSITE, PS50208; CASPASE_P20; 1.
 CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
 CC KW PROPEP 1
 CC PROPEP 1
 CC CHAIN 1
 CC CHAIN 29
 CC CHAIN 176
 CC ACT_SITE 121
 CC ACT_SITE 163
 CC ACT_SITE 163
 CC SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;
 CC
 CC Query Match 10.28; Score 183.5; DB 1; Length 277;
 CC Best Local Similarity 27.98; Pred. No. 1.2e-06;
 CC Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;
 CC
 CC 96 KSLDPPNNPREHVKKS-IQSEAF-PSGIPERKMKSKPLGICLID----- 144
 CC 11 KSKR---NEVKTIHSSKMSDGIYLDSE---YKMDYPMKGVITILNNKPKSTGM 61
 CC 145 --CIGNETEL-LRDTPTSLGYEVQKFLHSMGSIQIIGQAFKMEHEDYDSPVCVLS 200
 CC 62 TPRSGTDVDAKAKETWALKEVRANKNDLTRREIVELM-KNASKEDHKSRSFVCVILS 120
 CC 201 RGGSGSYGVGDQTHSGPLPHIRKPMFGDSCPLIAKPKKFFIC-NVYVSGQLDESL 258
 CC 121 HGDGVIIFGD---GPIDLKKITSYFRGDICRLIKPKLFIITQACRGTELCGISTDSG 177
 CC 259 LEVGGPMKKEVFAKQKGLCTVREADPFMSLCTADMSLLEQSHSPSLYIQCISQKLR 318
 CC 178 TEDDMTQCK-----IPVEDPLIYASTHFGYVSWMNPDSGFWIFQSLCSMLX 224

AC P42574; Q96AN1; Q96KP2;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A., AND VARIANT GLUT-190.
 RC TYSSUE-T-cell.
 RX MEDLINE=95074098; PubMed=7993002;
 RA Fernandez-Alnemati T., Litwack G., Alnemati E.S.;
 RT "CPP32, a novel human apoptotic protein with homology to
 RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
 RT Interleukin-1 beta-converting enzyme.";
 RL J. Biol. Chem. 269:30761-30764(1994).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95292347; PubMed=7774019;
 RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
 RA Beutler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
 RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
 RT protease that cleaves the death substrate poly(ADP-ribose)
 RT polymerase.";
 RL Cell 81:801-809(1995).
 [3]
 RN SEQUENCE FROM N.A.
 RA Vallette F.M., Oliver L.J.;
 RT "Control of the activation of the procaspase-3 by a sequence located
 RT at the N-terminus of the p17 subunit.";
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A., AND VARIANT GLUT-190.
 RP Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 [5]
 RN SEQUENCE FROM N.A., AND VARIANT GLUT-190.
 RP TISSUE=Lymph;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Matulis A.K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnanaprath P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Du X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schenck A., Schein U.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RN SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
 RX MEDLINE=95319529; PubMed=7596430;
 RA Nicholson D.W., Ali A., Thornberry N.A., Viallancourt J.P., Ding C.K.,
 RA Gallant M., Gareau Y., Griffin P.R., Labelle M., Lezeminik Y.A.,
 RA Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
 RA Miller D.K.;

RT "Identification and inhibition of the ICE/CED-3 protease necessary
RT for mammalian apoptosis.";
RT Nature 376:37-43(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=96266352; PubMed=8673606;
RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vallancourt J.P.,
RA Thornberry N.A., Becker J.W.;
RT "The three-dimensional structure of apopain/CPP32, a key mediator of
RT apoptosis.";
RT Nat. Struct. Biol. 3:619-625(1996).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RX MEDLINE=97197830; PubMed=9045680;
RA Mital P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
RA Priestle U.P., Tomaselli K.J., Gruetter M.G.;
RT "Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RT J. Biol. Chem. 272:6539-6547(1997).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20283632; PubMed=10821855;
RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
RA Levy M.A., Dewolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
RA Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RT inhibit apoptosis and maintain cell functionality.";
RT J. Biol. Chem. 275:16007-16014(2000).
RN [10]
RP PROCESSING.
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandez-Alnemir T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemir E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FAD-like domains.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [11]
RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kaichman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Estargani P., Thornberry N.A.;
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RT Nat. Genet. 13:442-449(1996).
RN [12]
RP FUNCTION.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kaichman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Estargani P., Thornberry N.A.;
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RT Nat. Genet. 13:442-449(1996).
RN [13]
RP RESPONSIBLE FOR APOPTOSIS EXECUTION. At the onset of apoptosis it
RN proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
RN 216-Asp-1-Gly-217 bond. Cleaves and activates steroid regulatory
RN element binding proteins (SRBPs) between the basic helix-loop-
RN helix leucine zipper domain and the membrane attachment domain.
RN Cleaves and activates caspase-6, -7 and -9. Involved in the
RN cleavage of huntingtin.
RN [14]
RP ENZYME REGULATION: Inhibited by isatin sulfoxamides.
RN [15]
RP SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
RN [16]
RP SUBCELLULAR LOCATION: Cytoplasmic.
RN [17]
RP TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
RN in testis. Also found in many cell lines, highest expression in
RN cells of the immune system.
RN [18]
RP PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
RN GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
RN PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
RN ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
RN OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
RN AND VICE VERSA.
RN [19]
RP SIMILARITY: Belongs to peptidase family C14.

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CC -----
DR EMBL: U13737; AAA5015.1; -;
DR EMBL: U13738; AAA5035.1; -;
DR EMBL: U26943; AAA74928.1; -;
DR EMBL: A2413269; CAC8886.1; -;
DR EMBL: A219866; CAC8886.1; -;
DR EMBL: BC016926; AAI16926.1; -;
DR PIR: A55315; A55315.
DR PDB: 1PAU; 07-JUL-97.
DR PDB: 1CP3; 24-DEC-97.
DR PDB: 1GFV; 23-JUN-00.
DR MEROPS: C14.003; -;
DR Genew: HGNC:1504; CASP3.
DR MIM: 60636; -;
DR GO: GO:0004208; F:caspase-3 activity; TAS.
DR GO: GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
DR GO: GO:0008629; P:induction of apoptosis by intracellular sig. .; TAS.
DR GO: GO:0009405; P:apoptogenesis; TAS.
DR InterPro: IPR002139; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; ILIBENZYM.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolyse; Thiol; protease; Zymogen; Apoptosis; Polymorphism;
KW 3D-structure. 1
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT VARIANT 190 190
FT VARIANT 190 190
FT CONFLICT 31 36
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 65
FT HELIX 67 80
FT TURN 81 82
Query Match 10.2%; Score 183.5; DB 1; Length 277;
Best Local Similarity 26.4%; Pred. No. 1.2e-06;
Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;
OY 98 LKPSNNFREPXYK-----KSIOSEPAFLPOSIPPERYKMSKPLGICILID----- 144
DB 1 MENTENSVBKSKIKNLEPKIHHGSEMSDGLSDSYKDDPFWGLCITINNKRFHKSSTG 60
OY 145 ---CIGNETEL---LRDTFSLGVEYQKFLHLSMHSIOILQFACMPERHSDYDFVCVLY 199
DB 61 MTRSGDPAANLRLTFNFKKXVFNKNDLREIIVELMDVS-KEDHSKRSPFVCLL 119
OY 200 SREGSOSVYGVDOTHSGLPLHHIRKRVMDSCPYLAGPKVFTIO--NYVSDGQLEDS 257
DB 120 SHEEBGIRF---TNPAPVLKRTTFRRDRSRSLTGKFKFIIDACRGTELDGIEIDS 176
OY 258 LLEVPDPAKKNVFEKQKRGKGLCTVREADPFSLCTAUMSLLEQSHSPSLYLQCLSQKL 317
DB 177 GVDDDMARK-----IPVDADFLYAYSTAGYYSWRNSKSGSFIQSLCML 223

Oy 318 RQ 319
 Db 224 KQ 225

RESULT 13

ICE2_MOUSE STANDARD; PRT; 435 AA.

AC P29594; 008737; (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 protein)
 GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA MEDLINE=9504733.9; PubMed=7958843;
 RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
 RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a protein similar to the product of the Caenorhabditis elegans cell death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
 RT Genes Dev. 8:1613-1626(1994).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RA MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I., van Looy G., Mollema F., Schotte P., van Crickinge W., Beyaert R., Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RT FEBS Lett. 403:61-69(1997).
 RL [3]
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=92328780; PubMed=1378265;
 RA Kumar S., Tomooka Y., Noda M.;
 RT "Identification of a set of genes with developmentally down-regulated expression in the mouse brain.";
 RT Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
 RL [4]
 RP FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival. May be important in multistep carcinogenesis.
 CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By similarity).
 CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic CNS, liver, lung, kidney, small intestine, and hair follicles of vibrissae. Moderate expression seen in the skin, oral mucosa, skeletal muscle, submandibular gland and thymus. In the adult, it is highly expressed in spleen, lung and kidney. Moderately in the brain, heart, testis, liver. Low levels in the thymus, skeletal muscle, ovary and gut.
 CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly expressed in several types of mouse tissue undergoing high rates of programmed cell death such as central nervous system and kidney.
 CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 1 CARD domain.
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 CC -----

DR EMBL: D28492; BAA25876.1; ALT_INIT.
 DR EMBL: Y13085; CAA73527.1; ALT_INIT.
 DR HSSP: P42574; ICP3.
 DR MEROPS: C14.006; --.
 DR MED: MG1:97295; Casp2.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00619; CASP; 1.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PRO0376; ILBENZYM.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR Hydrolase; Thiol protease; Apoptosis; Zymogen.
 FT PROPEP 1 152
 FT CHAIN 153 316
 FT CHAIN 317 435
 FT CHAIN 331 435
 FT DOMAIN 15 103
 FT ACT_SITE 260 260
 FT ACT_SITE 303 303
 FT ACT_SITE 303 303
 FT CONFLICT 71 71
 SQ SEQUENCE 435 AA; 48896 MW; 89846AA76E7A676 CRC64;
 Query Match 10.0%; Score 179.5; DB 1; Length 435;
 Best Local Similarity 21.5%; Pred. No. 4,1e-06;
 Matches 87; Conservative 59; Mismatches 137; Indels 121; Gaps 14;

Oy 42 LKRLNVAPDOU---DLLEKCL-KNIHRIDLTXTIQ---KYSQVQAGTSYRNVLQA- 92
 Db 23 LKKNRYVLAKQKLLSLLEHLLEKDIITLEMRELLQAKGSGSVNVELNLTPKRGPOAF 82
 Oy 93 -AIQSLKQDPSNNFRPEPVKKSIOSEAFLP-----QSIPER----- 129
 Db 83 DAFCEALRETRQGHLEDLTLTSLDIQHVLPPLSCDDYDTSLPFVSCSCPPHKQURLSTD 142
 Oy 130 -----YKMSKPLGICLIIDCI----- 146
 Db 143 ATSHSLDNGDPCLLVKCTEPFYQAHYQLARLOSQPRGLALVLSNVHFTGEKDLFR 202
 Oy 147 -GNETE--LIRDTFTSLGYEVQKFLHLSWNGISQILQCPACMPERRDYDSFVCYVSKGG 203
 Db 203 SGGDVHTTLVTLFKLGYNVHLDQTAQOEKQLQFAQLPARVYDSCVALLSHGV 262
 Oy 204 SQGVYGVDDHSHSLPLHHRBMFMGDCPYLAGKPMFPIQ-----NY 246
 Db 263 EGGIYVD--GKLLQLOQVFRFLPDNANCSSLQNKRMFTIQACREDDETRGVQDDGKNH 320
 Oy 247 VVSDQQLBDS---LLEVDPAMK-----NVFKAQKQGLCTVHREADFWSL 291
 Db 321 TQSGCESDAGAEELMKRLPFRSDMTCGYACLKNAMRMTKSGSWYIEALTQVF--SE 379
 Oy 292 CTADMSLLEQSHSPSLVYIQCSQKRCRGRTIPGSGITSEKDM 335
 Db 380 RACDMHVAWM-----LVKNVALIKEREYAGTEFRCKEM 415

RESULT 14

ICE2_HUMAN STANDARD; PRT; 435 AA.

ID ICE2_HUMAN
 AC P42575; P42576;
 DT 01-NOV-1995 (Rel. 32, Created)

QY 264 -----PAMKNVEFFKQKGLCTVHEADPFWSLCTADNLSLEQSHSPSLYLQCLSQ-- 315
 Db 318 KNAAGSGCEESDAGKELPKMELPTRSDMICGYACLTCTAMNTKSGWYIELAQVF 377
 QY 316 -----KLRGERGTPGSGITRESKDM 335
 Db 378 SERACDMVADMLVKYNALIKREGYAFGTFRCKEM 415
 RESULT 15
 ICE6_MOUSE STANDARD; PRT; 276 AA.
 ID ICE6_MOUSE
 AC 008738;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
 DN CASP6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
 RA van Loo G., Wollemans F., Schotte P., van Crieginge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 FEBS Lett. 403:61-69(1997).
 CC -! FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Cleaves poly(ADP-ribose)
 polymerase in vitro, as well as lamins. Overexpression promotes
 programmed cell death (By similarity).
 CC -! SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
 (By similarity).
 CC -! SUBCELLULAR LOCATION: Cytoplasmic.
 CC -! TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
 testis, and heart. Lower levels in spleen, skeletal muscle and
 brain.
 CC -! PTM: CLEAVAGES BY CP932, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
 SUBUNITS (BY SIMILARITY).
 CC -! SIMILARITY: Belongs to peptidase family C14.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y13087; CA073529.1; -.
 DR HSSP; P42574; IPRU.
 DR MEROPS; C14.005; -.
 DR MCD; MGI:1312921; Casp6.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; ILIBENZTME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50209; CASPASE_P20; 1.
 KM Hydrolase; Thiol protease; Apoptosis; Zymogen.
 FT PROPEP 1 5
 FT CHAIN 6 162 BY SIMILARITY.
 FT PROPEP 163 176 CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
 FT CHAIN 177 276 CASPASE-6 SUBUNIT P11 (BY SIMILARITY).

FT ACT_SITE 104 104 BY SIMILARITY.
 FT ACT_SITE 146 146 BY SIMILARITY.
 SQ SEQUENCE 276 AA; 31595 MW; 5965DB9321126B6C CRC64;
 Query Match 9.6%; Score 172.5; DB 1; Length 276;
 Best local Similarity 27.8%; Pred. No. 7.7e-06;
 Matches 62; Conservative 26; Mismatches 84; Indels 51; Gaps 8;
 QY 126 PERRYMKKPKFGICLIID-----CIGNTELLRDFITSLGYEYOKF----- 167
 Db 16 PABQYMDHKRRGVALLIFNHERFFWHLTLPERGNTAARDNITRRFSGLGEVXCFNDLR 75
 QY 168 ---LHLSMHGISQILGQFACMPEDRDYDFVCVLVSRGASQSVYGV-----QTHSGIPL 219
 Db 76 AEELLKIHVS-----TSHIDADQFICVFLSHGKGNHVAVDKIRIQLTGL-- 125
 QY 220 HIRRMFMGDSCEPYLAGKPMFFIQLNYVYVSGQLDSSILEYD-----GPMKNVEFFKQ 274
 Db 126 -----FKDICKCSLVGKPKIFIIQ---ACRSGQHDVPVPLDWDHQDTKLDNVT--QVD 175
 QY 275 KRGICTVHEADPFWSLCTADNLSLEQSHSPSLYLQCLSQCL 317
 Db 176 AASVYTLIPAGADPLMICYVAEGYSHREIVNGSWYIQLCEML 218

Search completed: September 8, 2004, 05:49:01
 Job time : 16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2004, 05:48:38 ; Search time 46 Seconds
(without alignments)
2386.964 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800
Sequence: 1 MARI6DLKDPVSLIFLM.....ITKXDMHFSIGCIILDLV 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP_mbc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriaph:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	1774	98.6	462	4	Q96TE4	Q96TE4	homo sapien
2	1018	56.6	481	11	Q812G4	Q812G4	mus musculus
3	471	26.2	418	13	Q8UVG5	Q8UVG5	brachydanio
4	345	19.2	218	11	Q9JWZ5	Q9JWZ5	rattus norv
5	318.5	17.7	482	11	Q9JHX4	Q9JHX4	rattus norv
6	302.5	16.6	482	13	Q90XU1	Q90XU1	gallus gall
7	277	15.4	78	6	Q8M1I8	Q8M1I8	maca mla
8	267	14.8	520	6	Q91B62	Q91B62	xenopus lae
9	265.5	14.8	476	13	Q91B73	Q91B73	brachydanio
10	248.5	13.8	522	4	Q81UP5	Q81UP5	homo sapien
11	233	12.9	500	13	Q91B64	Q91B64	xenopus lae
12	214	11.9	283	13	Q93A17	Q93A17	gallus gall
13	210.5	11.7	496	5	Q81749	Q81749	suberites d
14	199	11.1	303	13	Q91B66	Q91B66	xenopus lae
15	198.5	11.0	400	5	Q817P2	Q817P2	branchio
16	193.5	10.8	277	6	Q95ND5	Q95ND5	sus scrofa

17	192.5	10.7	318	13	Q91B65	Q91B65	xenopus lae
18	192	10.7	277	6	Q8WK15	Q8WK15	canis famli
19	190.5	10.6	313	11	Q8CHV5	Q8CHV5	mus musculus
20	190	10.6	328	5	Q81TP3	Q81TP3	branchio
21	189.5	10.5	277	6	Q8XU1	Q8XU1	felis silve
22	187.5	10.4	302	13	Q91B69	Q91B69	oncorhynch
23	186.5	10.4	280	13	Q81B59	Q81B59	oryzias lat
24	184.5	10.2	182	6	Q77623	Q77623	ovis aries
25	184	10.2	290	13	Q81J58	Q81J58	oryzias lat
26	182.5	10.1	304	13	Q93415	Q93415	gallus gall
27	180.5	10.0	452	11	Q55194	Q55194	rattus norv
28	179.5	10.0	452	11	Q8K241	Q8K241	mus musculu
29	179.5	10.0	452	11	Q8C9H7	Q8C9H7	mus musculu
30	179	9.9	423	13	Q91B67	Q91B67	xenopus lae
31	177.5	9.9	277	6	Q8MUP3	Q8MUP3	oryctolagus
32	177.5	9.9	435	4	Q9HUP7	Q9HUP7	homo sapien
33	172.5	9.6	276	11	Q9D089	Q9D089	mus musculu
34	172.5	9.6	276	11	Q9M47	Q9M47	mus musculu
35	172.5	9.6	280	13	Q8U42	Q8U42	figu rubrip
36	172.5	9.6	415	13	Q801W6	Q801W6	xenopus lae
37	172.5	9.6	419	13	Q72XD2	Q72XD2	xenopus lae
38	172	9.6	277	11	Q35397	Q35397	rattus norv
39	172	9.6	343	11	Q9MUT6	Q9MUT6	rattus norv
40	170.5	9.5	280	13	Q8JGM9	Q8JGM9	figu rubrip
41	169	9.4	312	4	Q8EUT3	Q8EUT3	homo sapien
42	166.5	9.2	289	5	Q8EFL0	Q8EFL0	anopheles s
43	165	9.2	303	11	Q88550	Q88550	rattus norv
44	158.5	8.8	282	13	Q98U18	Q98U18	brachydanio
45	152.5	8.5	182	12	Q99CX0	Q99CX0	bovine herp

ALIGNMENTS

RESULT 1

ID	Q96TE4	PRELIMINARY;	PRT;	462 AA.
AC	Q96TE4	Q96TE4	Q96TE4	Q96TE4
DT	01-DEC-2001	(TEMBLrel. 19, Created)		
DT	01-DEC-2001	(TEMBLrel. 19, Last sequence update)		
DT	01-OCT-2003	(TEMBLrel. 25, Last annotation update)		
DE	Usurpin beta.			
OS	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEBLINE-21100893; PubMed=1161814;			
FA	Hadano S., Yanagisawa Y., Skrag J., Fichter K., Nasir J.,			
FA	Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,			
RA	Ikeeda J.-E., Hayden M.R.,			
RT	"Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,			
RT	and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)			
RT	critical region at chromosome 2q33-q34: Candidate genes for ALS2.";			
RL	Genomics 71:200-213 (2001).			
DR	EMBL; AB038967; BAB32552.1; -			
DR	EMBL; AB038967; BAB32552.1; JOINED.			
DR	EMBL; AB038968; BAB32552.1; JOINED.			
DR	EMBL; AB038969; BAB32552.1; JOINED.			
DR	EMBL; AB038970; BAB32552.1; JOINED.			
DR	EMBL; AB038971; BAB32552.1; JOINED.			
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.			
DR	GO; GO:0030693; F:caspace activity; IEA.			
DR	GO; GO:0006955; P:apoptosis; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR001875; ICD.			
DR	InterPro; IPR001309; ICE_P20.			
DR	InterPro; IPR002398; Peptidase_C14.			
DR	Pfam; PF01335; DED; 2.			
DR	Pfam; PF00666; Peptidase_C14; 1.			
DR	SMART; SM00115; CASC; 1.			
DR	SMART; SM00031; DED; 2.			

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DR PROSITE; PSS0208; CASPASE_P20; 1.
DR PROSITE; PSS0168; DED; 2.
SQ SEQUENCE 462 AA; 52550 MW; DAED0109CEAA7EAA3 CRC64;

Query Match
Best Local Similarity 98.6%; Score 1774; DB 4; Length 462;
Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSVSSLIIFLMKDYNGRGKISKEKSPFLDLYVELEKLNVAPODLDLEKCL 60
DB 97 MAEIGEDLDKSVSSLIIFLMKDYNGRGKISKEKSPFLDLYVELEKLNVAPODLDLEKCL 156
QY 61 KNHRIIDLTKRIQKTKQKQSVGAGTSYRNVLOAAIQKSLKDPSSNFRFLHNRSKQKRLKEQ 216
DB 157 KNHRIIDLTKRIQKTKQKQSVGAGTSYRNVLOAAIQKSLKDPSSNFRFLHNRSKQKRLKEQ 216
QY 107 ---EEPVKKSQSESAFLPOSIPERRYKMSKPLGICLIIDICGNTELLRDTFTSLGY 162
DB 217 LGAOCEPVKKSQSESAFLPOSIPERRYKMSKPLGICLIIDICGNTELLRDTFTSLGY 276
QY 163 EVQKFLHSMHGISQILQGFACMPHRDYSFVCVLVSRGSGSVYGVDTGSLPLHHI 222
DB 277 EVQKFLHSMHGISQILQGFACMPHRDYSFVCVLVSRGSGSVYGVDTGSLPLHHI 336
QY 223 REMFGDSCPYLAGKPKMFFIQNYVSDGQLEDSSLEVDGPAMKRVFKAQRGLCTVH 282
DB 337 REMFGDSCPYLAGKPKMFFIQNYVSDGQLEDSSLEVDGPAMKRVFKAQRGLCTVH 396
QY 283 RADFFWSLCTADMSLLEQSHSSPSLYIQCLSQKLRQERTIRGSGITTEKDMHSSLG 342
DB 397 RADFFWSLCTADMSLLEQSHSSPSLYIQCLSQKLRQERTIRGSGITTEKDMHSSLG 456
QY 343 ILLDYL 348
DB 457 ILLDYL 462

RESULT 2
ID Q812G4 PRELIMINARY; PRT; 481 AA.
AC Q812G4;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CASP8 and FADD-like apoptosis regulator.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Strausberg R.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR001309; ICS_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR SMART; SM00115; CASc; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PSS0208; CASPASE_P20; 1.
DR PROSITE; PSS0168; DED; 2.
SQ SEQUENCE 481 AA; 54874 MW; 43E07E2E5FA5A05 CRC64;

Query Match
Best Local Similarity 56.6%; Score 1016; DB 11; Length 481;
Matches 211; Conservative 41; Mismatches 67; Indels 18; Gaps 5;

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QY 1 MAEIGEDLDKSVSSLIIFLMKDYNGRGKISKEKSPFLDLYVELEKLNVAPODLDLEKCL 60
DB 102 LMEIGESLDNDVSLVFLTRDYTGKIAKDSFPLDLYVELEKLNVAPODLDLEKCL 161
QY 61 KNHRIIDLTKRIQKTKQKQSVGAGTSYRNVLOAAIQKSLKDPSSNFRFLHNRSKQKRLKEQ 216
DB 162 KNHRIIDLTKRIQKTKQKQSVGAGTSYRNVLOAAIQKSLKDPSSNFRFLHNRSKQKRLKEQ 216
QY 110 ---YKKSQSESAFLPOSIPERRYKMSKPLGICLIIDICGNTELLRDTFTSLGYEV 164
DB 221 SQTFLVXTSIOESGAFIPHIREIYRMOSKPLGICLIIDICGNTELLRDTFTSLGYH 280
QY 165 QKFLHSMHGISQILQGFACMPHRDYSFVCVLVSRGSGSVYGVDTGSLPLHHI 224
DB 281 QKFLHSMHGISQILQGFACMPHRDYSFVCVLVSRGSGSVYGVDTGSLPLHHI 340
QY 225 MFMGDSCPYLAGKPKMFFIQNYVSDGQLEDSSLEVDGPAMKRVFKAQRGLCTVH 284
DB 341 MFTGDTCPSLRGKPKLFFIQNYVSDGQLEDSSLEVDGPAMKRVFKAQRGLCTVH 399
QY 285 ADFFWSLCTADMSLLEQSHSSPSLYIQCLSQKLRQERTIRGSGITTEKDMHSSLG 342
DB 400 ADFFWSLCTADMSLLEQSHSSPSLYIQCLSQKLRQERTIRGSGITTEKDMHSSLG 436

RESULT 3
ID Q8UVG5 PRELIMINARY; PRT; 418 AA.
AC Q8UVG5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Clarp1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96021435; PubMed=9380701;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "Clarp, a death effector domain-containing protein interacts with
RT caspase-8 and regulates apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448261; AL41007.1; -
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR001309; ICS_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR SMART; SM00115; CASc; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PSS0208; CASPASE_P20; 1.
DR PROSITE; PSS0168; DED; 2.
SQ SEQUENCE 418 AA; 47619 MW; C2ECB3AE571E0237 CRC64;

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RESULT 6
Q90WU1 PRELIMINARY; PRT; 482 AA.
ID Q90WU1
AC Q90WU1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase 8.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Barton S., Bridgman J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY057939; AAL23700.1; -.
DR MEROPS: C14.009; -.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0030693; F:caspase activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002138; ICD_p10.
DR InterPro: IPR001309; ICD_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF01335; DED; 2.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; IL1BCENZYM.
DR SMART: SM00031; DED; 2.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR PROSITE: PS50168; DED; 2.
SQ SEQUENCE 482 AA; 54645 MW; 8E3936BE8E090BBF CRC64;

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Query Match 16.8%; Score 302.5; DB 13; Length 482;
Best Local Similarity 25.9%; Pred. No. 6.3e-16;
Matches 89; Conservative 67; Mismatches 141; Indels 47; Gaps 10;

QY 3 EIGEDLDKSDVSSILFLMKDYGRKTSKESFLDLVLEKLNLAAPQLDLLEKCLN 62
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 107 QLEENITKDMKCKEFLGKELPRCKLSPTTMPDVLEMEKGLIKENLVTKTICK 166
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 63 IHRIDLTQIKYKQSVQAGTSYRNVLOAIIQKSLKDPNNFRBPVKKSIOESAFIP 122
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 167 VDKSLK-KIDYEINLNGEG-----EMLVTEGORSSTGAPEDSAIWLASSVAP 214
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 123 QSIPE-----ERYKMSKPLGICLI-----DCIGN--ETELLR 154
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 215 DSLGNCDSQLELYYKNTSRPRGYCLLNHNPAKAREAVPELRMKDNGHTVADALR 274
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 155 DTFTSLGYEOKFLHLSNHSIQLLGFPACMPEHRDYDSVCLVSRGSGSVYGVQTH 214
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 275 KVFSTLHFTVAEYDCTEEIRNTVNNYRCM-DHNNDKDCVCCILSHGKKDIIYGVQGE 333
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 215 SGLPLHNRMFMDSCGYLAGKRPFIQNYVYSDQGLDSSLLVD--GPMKNVEFA 273
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 334 --VPQELTTFTGNCOSLAGKPKFFVQ--ACQGDAYKGVTTITDSGEODYSLEIDA 389
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 274 QKRGICTVHREADFFWSLCTADMSLBSQSSSPLYLQCSQRL 317
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 390 RFOIDC-IPSEADFLGNTTIQDVVSYSRSPSGTWYISQICQL 432
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 7
Q8MJ18

PRELIMINARY; PRT; 78 AA.

```

Q8MJ18;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Flice/caspase-1 inhibitory protein (Fragment).
OS Macaca mulatta (Rhesus macaque)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Morceaux V., Ho Tsong Pang R., Hurtrel B., Ameisen J.-C.,
RA Escarguer J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF530077; AAM95637.1; -.
DR NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 78 AA; 8971 MW; 6BD2080957331A99 CRC64;

Query Match 15.4%; Score 277; DB 6; Length 78;
Best Local Similarity 73.1%; Pred. No. 7.3e-15;
Matches 57; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 86 YRNVLOAIIQKSLKDPNNFR-----EPPVKSIOSEAFIPQSIPE 127
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 YKRVLOAIIQKSLKDPNNFRLNHNGRSKEORLKEQLGTQEPVKTSSIOSEAFIPQSIPE 60
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 128 ERYKMSKPLGICLIIDC 145
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 ERYKMSKPLGICLIIDC 78
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 8
Q91B62
ID Q91B62 PRELIMINARY; PRT; 520 AA.
AC Q91B62;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-10.
GN XCASPASE-10.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:20209426; PubMed:10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL: ABO38173; BA94751.1; -.
DR HSPB: O15806; 10DU.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0030693; F:caspase activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001875; DED.
DR InterPro: IPR001875; DED.
DR InterPro: IPR002138; ICD_p10.
DR InterPro: IPR001309; ICD_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF01335; DED; 2.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; IL1BCENZYM.
DR SMART: SM00031; DED; 2.

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ID	PRELIMINARY	PRT	AA
0918b3			
0918b3			
0918b3			
01-OCT-2000	(TREMBLrel. 15, Created)		
01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
Caspase-8.			
CASP8.			
Brachydanio rerio (zebrafish) (Danio rerio).			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
Cyprinidae; Danio.			
NCBI_TaxId=7955;			
[1]			
SEQUENCE FROM N.A.			
MEDLINE=20373792; PubMed=10917738;			
Inohara N., Nunez G.;			
"Genes with homology to mammalian apoptosis regulators identified in			
zebrafish.";			
Cell Death Differ. 7:509-510(2000).			
EMBL; AF273220; AAF79207.1; -			
HSSP; Q15806; 10DU.			
MEROPS, C14.009; -.			
ZFIN; ZDB-GENE-000713-1, casp8.			
GO; GO:0016329; F:apoptosis regulator activity; IEA.			
GO; GO:0030693; F:caspace activity; IEA.			
GO; GO:0006915; F:apoptosis; IEA.			
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
InterPro; IPR001875; DEN.			
InterPro; IPR002138; ICF_p10.			
InterPro; IPR001309; ICF_p20.			
InterPro; IPR002398; Peptidase C14.			

```

QY      1 MEIGEDDLKSVSSLIETPMMDYMRGKISKESEKFLDVALEETYNVADPOD---IL 56
D      103 LKLSIDMTIEHFRAKFLD--LPRALGNSSTFDLALIMEGQRLGPDNDIELVRIL 166
QY      57 ECKLNHRIIDLTKYIKYKOSVQAGTSYNYTQAAIQSLKDPNNPFEPRYKSIQE 116
D      161 ECKDKLAWIERFNQSHROEOGRPLLEEVF--LNNPVSOTMERERRRNSAGAIT 217
QY      117 SEAFLOSIPERERYAKSKPLGICLIIDICG--NETELNRDT-----FTSLGY 162
D      218 TDAEPFLN--FNYYIILTLQRPGLCYLIINNVNFEISTNLKRTGDMOKRLAKFSMHF 276
QY      163 EYQKFLHSMGHSIQILOQFACMFENRHDYDFVCYLVNRSQSSQYVGVDOHSLP--LH 220
D      277 QLEVRNDELAIAIKETIKQFA--NRYHSMGFAVCCILSHGKKGVLGTD---GKPEIR 331
QY      221 HIRRMEDSCPYLNGKPRMFEIQNYVVSDDQLDLSLLEVDG--PAKVNFEAKQKGL 278
D      332 EYVLPFAG--CRTLSKRPFLFIQ---ACQGDENQAGVWTSIDGSEDPAPEDEEYEDAGI 386
QY      279 CYVHR---EADFFMSLCTADMSLLEQSHSPSYLIQCLISQTLRQ 319
D      387 IYRKIPLEADFLIGNAIVENHLSFRATYKKSITFIQELCKMEE 430

```

```

RESULT 10
081UPS
ID 081UPS          PRELIMINARY;          PRT;          522 AA.
AC 081UPS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 10, apoptosis-related cysteine protease.
OS Homo sapiens (human).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Straussberg R.;
RL Submitted (YAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042844; AAH42844.1; -.
DR GO; GO:0016129; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; TLBCEZYME.
DR SMART; SMO0115; CASc; 1.
DR SMART; SMO0031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR

```


RESULT 15

08ITP2 PRELIMINARY; PRT; 400 AA.
AC 08ITP2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE AmphicASP-6.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN (1)
RP SEQUENCE FROM N.A.
RA Bayasas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,
RA Comella J.X.,
RT "Isolation of AmphicASP-6, an amphioxus (Branchiostoma floridae)
RT caspase-6 homolog containing a Pyrin prodomain."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF412336; AAN45850.1; -
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICB_P10.
DR InterPro; IPR001309; ICB_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1HCENZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 400 AA; 44309 MW; 5C3B1B813E73DFAE CRC64;

Query Match

11.0%; Score 198.5; DB 5; Length 400;

Best Local Similarity 26.8%; Pred.No.1,1e-07;
Matches 73; Conservative 44; Mismatches 116; Indels 39; Gaps 10;

QY 76 KQSVQAGTSTRNVIQAIQKSLKDPNNFREPVKKSIOESFAFLPQSIPEERYKMKSK 135
DB 93 KEVCLGPGHAEKVTVDSSQEQDEPDAPYISIVRRAPQAE--LLQDLPS--YNNNP 148
QY 136 PIGLICLIIDCIGNE-----TEL-----LRDFTSLGVEYOKFLHSMGISOI 178
DB 149 QRGELCLVPD--NEEFHTTKNNRRRGSHVDAGNLKMFEGLGFSVEVLKDKETETROI 205
QY 179 LGOFAKPEHRDYDSFVCLVSRGQSOSVYGVDQTHSGPLPHIIRKVFMDSCPYLAGKP 238
DB 206 LHSALKYDHSQDQCFVFLSHGEDGMIYGVNLT--VPIKETDVFRAFRCTSLKGP 262
QY 239 KMFETQ-----NYVVSQDLDDSSILFVDGPA--MKNVKFAKRGGLCTHREADPFMSL 291
DB 263 KLFETQACRGAKHEIPVEPLDEPDGLBSGSAEPMDVVDAGVPR---TLPAGADFLMAY 318
QY 292 CTADMSLLEQSHSPSLYLQCLISQLRQERGT 323
DB 319 SVSEGFYSHRDVTNGSWYVQDLCAALKQ-HGT 349

Search completed: September 8, 2004, 05:51:28
Job time : 55 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2004, 06:24:47; Search time 40 Seconds

(without alignments)
836.866 Million cell updates/sec

Title: US-10-713-208-6

Sequence: 1 MAEIGDLDKSDVSSLIPLM.....ITBSKDXHFFSLGICLLDVL 348

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 180989

Minimum DB seq length: 0

Maximum DB seq length: 348

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 78:1*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184.5	10.2	212	2 167437	cysteine proteinase
2	184.5	10.2	277	2 S64710	cysteine proteinase
3	184.5	10.2	277	2 JCS410	CPP32 protein - mo
4	183.5	10.2	277	2 A55315	cysteine proteinase
5	169	9.4	312	2 B54821	apoptosis regulator
6	149.5	8.3	182	2 167436	interleukin-1-beta
7	124.5	6.9	311	2 B56084	interleukin-1-beta
8	122	6.8	241	2 T30761	hypothetical prote
9	120	6.7	263	2 C56084	interleukin-1-beta
10	94.5	5.2	344	2 B70136	flagellar motor sw
11	89.5	5.0	184	2 A71230	hypothetical prote
12	89.5	5.0	265	2 AE0230	GnFR-family probab
13	88.5	4.9	168	1 A64478	hypothetical prote
14	88.5	4.9	208	2 A56912	PAAD protein - num
15	86.5	4.8	259	2 A71890	hydroxyethylthiaz
16	85	4.7	293	2 JCS410	3(or 17)beta-hydro
17	84	4.7	247	2 T33654	hypothetical prote
18	84	4.7	319	2 B86615	PP-loop type ATPas
19	84	4.7	319	2 E72809	Mead/cf6f family
20	83.5	4.6	301	2 A70335	hypothetical prote
21	82.5	4.6	324	2 C83695	quinone oxidoreduc
22	82	4.6	265	2 S70247	hypothetical prote
23	81.5	4.5	252	2 AE1885	HeaA protein limpo
24	81.5	4.5	266	2 T01482	hypothetical prote
25	81.5	4.5	168	2 S65215	hypothetical prote
26	81	4.5	173	2 S65215	hypothetical prote
27	81	4.5	317	2 B71922	probable sideropho
28	81	4.5	318	2 E70117	membrane fusion pr
29	81	4.5	324	2 F64592	hypothetical prote

30	80.5	4.5	171	2 S55668	hypothetical prote
31	80.5	4.5	242	2 UC7517	caspase-14/a - hum
32	80.5	4.5	292	1 A40650	urp-glucose-1-phos
33	80.5	4.5	308	2 B97263	tagatose-6-phospha
34	80.5	4.5	313	2 S51754	NSP3 protein - por
35	80.5	4.5	331	2 A71870	integrase/recombin
36	80	4.4	217	2 H90217	SSU ribosomal prot
37	80	4.4	238	2 C69157	recombinase - Meth
38	80	4.4	279	2 H97934	transcription anti
39	80	4.4	314	2 T25372	hypothetical prote
40	79.5	4.4	184	2 T07440	H+-transporting tw
41	79.5	4.4	267	2 A32122	dolichyl-phosphate
42	79.5	4.4	313	2 S51753	NSP3 protein - por
43	79.5	4.4	315	2 C82425	sensor histidine kin
44	79	4.4	197	2 G64329	anthranilate synth
45	79	4.4	279	2 A95067	transcription anti

ALIGNMENTS

RESULT 1
167437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C/Accession: I67437
R/Flaws: J.A.; Kugu, K.; Trbovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfeld, A.N.; Til
Endocrinology 136, 5042-5053, 1995
A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nosa cells of the ovarian follicle.
A/Reference number: 153300; MUID:96042508; PMID:7588240
A/Accession: I67437
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-212 <RES>
A/Cross-references: EMBL:U34685; NID:g1004370; PIDN:AA052261.1; PID:g1004371
C/Keywords: cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 212;
Best local similarity 29.1%; Pred. No. 7.2e-07;
Matches 60; Conservative 36; Mismatches 81; Indels 29; Gaps 8;

QY	127	EEHYKXKSPKLCILID-----CIGNETEL---IRDFTSLGIVYQKFLISM 172
DB	5	DSGYKMDYEMGLCIINKNFKSTGMSARNGDVIDANIRFTFMALKYEVNRKNDLTR 64
QY	173	HGISQILGFCACMPHHRDVSFVCYLVRGGSQSYGVQDTHSGPLHIRMFWGDCSP 232
DB	65	BEIMEIMDSVS-KEDHSKRKSFVCYLISHGDEGVIFG---TNGPVDLKKLTSFRGDYCR 120
QY	233	YLAGKPMFFIIONVYVSDQLEDSILLEVDPAMKNVEFKQKQGLCTVHREADPFWSLC 292
DB	121	SLTGKPKLFIO--ACRGETLDSG-IETDSGADDDV--ACQKRV-----EADFLVAYS 169
QY	293	TADMSLLEQSHSPSYVQLCSQKLR 318
DB	170	SAPGYSWRNSRSGSWFIQSLCAMLK 195

RESULT 2
S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C/Species: Citreululus griseus (Chinese hamster)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C/Accession: S64710; S72395
R/Flaws: X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A/Title: Cleavage of sterol regulatory element binding proteins (SRBPs) by CPP32 during
A/Reference number: S64710; MUID:96183185; PMID:8605870
A/Accession: S64710
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA

A:Residues: 1-277 <MAN>
 A:Cross-references: EMBL:U27463
 R:Wang, X.
 Submitted to the EMBL Data Library, May 1995
 A:Reference number: S72395
 A:Accession: S72395
 A:Molecule type: mRNA
 A:Title: 'A', '81-146', 'Y', '148-277' <MAN>
 A:Cross-references: EMBL:U27463; NID:g1244443; PDB:AA01511.1; PID:g1244444
 C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 27.9%; Pred. No. 1e-06;
 Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

QY 96 KSLDPSNNPREEPVKS-IOESAFIPQSIPEERYKMKSPKIGICLIID----- 144
 DB 11 KSIK---NFEVKTIHSGSKMSDGIYLDSS---YKMDYPEMGVCIITNNKPKHSTGM 61
 QY 145 --CIGNETEL--LRDFTSLGVEYQKFLHSMHGISOILGQFACMPEHRDYDSFVCVLVS 200
 DB 62 TPRSGTDVDAKLETETMNLKYVRNKNIDLREIYELWM-KNKSXEDHKSRSFVCVLVS 120
 QY 201 RGSQSQVYGVDTHTSGPLHHIRRMFGDSCPYLAGKPKFFITQ--NYVSDGQLEDSSL 258
 DB 121 HGDEGVIFGTD---GPIDLKLTISYFRGDRCRSLTGKPKLFIIOACRGTELDGIEITDSG 177
 QY 259 LEVDGPAKKNVEFKAQKRGKGLCTVHREADPFWSLCTADMSLLBQSHSSPSLYLQCLSQKLR 318
 DB 178 TEDVYTCOK-----IPEADPLVAYSTAPGYYSWRNKSQSWFIQSLCSMLK 224

RESULT 3
 JCS410
 CP32 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
 C:Accession: JCS410
 R:Okada, T.; Urae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 Biochem. Biophys. Res. Commun. 231, 170-174, 1997
 A:Title: Specific expression of CP32 in sensory neurons of mouse embryos and activation
 A:Reference number: JCS410; MUID:97224429; PMID:9070890
 A:Accession: JCS410
 A:Status: nucleic acid sequence not shown
 A:Residues: 1-277 <MO>
 A:Molecule type: mRNA
 A:Cross-references: DDBJ:D86352
 A:Experimental source: embryo
 C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 10.2%; Score 184.5; DB 2; Length 277;
 Best Local Similarity 28.9%; Pred. No. 1e-06;
 Matches 67; Conservative 35; Mismatches 93; Indels 37; Gaps 11;

QY 103 NNPREEPV--KXSQESAPFLPQSIPEERYKMKSPKIGICLI-----DCIGN 148
 DB 14 NNFQVKTTHGSKSV-DSGIYLDSS-----YKMDYPEMGICITITNNKPKHSTGMSSRSGT 67
 QY 149 ETEL--LRDFTSLGVEYQKFLHSMHGISOILGQFACMPEHRDYDSFVCVLVSRRGSOS 206
 DB 68 DVDANLRETFMGKLYVRNKNIDLREIYELMDVS-KEDHKSRSFVCVLISHGDEGV 126
 QY 207 VYGVDTHTSGPLHHIRRMFGDSCPYLAGKPKFFITQ--NYVSDGQLEDSSLLEVDPAM 266
 DB 127 IFG---TNGPVDLKKLTISYFRGDRCRSLTGKPKLFIITQ--ACRGTELDG--LEHDSG-- 178
 QY 267 KNVEFKAQKRGKGLCTVHREADPFWSLCTADMSLLBQSHSSPSLYLQCLSQKLR 318
 DB 179 -DEEMACQK-----IPEADPLVAYSTAPGYYSWRNKSQSWFIQSLCSMLK 224

RESULT 4
 AS5315

cysteine proteinase (EC 3.4.22.-) CP32 precursor - human
 N:Alternate names: cysteine proteinase CP32
 C:Species: Homo sapiens (man)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
 C:Accession: A55315; S58899; I39005
 R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
 J. Biol. Chem. 269, 30761-30764, 1994
 A:Title: CP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
 A:Reference number: A55315; MUID:95074098; PMID:7983002
 A:Accession: A55315
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-277 <PER>
 A:Cross-references: GB:U13737; NID:S561665; PDB:AAA65015.1; PID:9561666
 R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant,
 J. Yu, V.L.; Miller, D.K.
 Nature 376, 37-43, 1995
 A:Title: Identification and inhibition of the ICE/ced-3 protease necessary for mamma
 A:Reference number: S58899; MUID:95319529; PMID:7596430
 A:Accession: S58899
 A:Molecule type: protein
 A:Residues: 29-46; 176-189; 'E', '191-193' <NIC>
 R:Twari, M.; Quan, L.T.; O'Rourke, K.; Deeneyers, S.; Zeng, Z.; Beidler, D.R.; Poite
 Cell 81, 801-809, 1995
 A:Title: Yama/CP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
 A:Reference number: A56924; MUID:95292347; PMID:7774019
 A:Accession: I39005
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-189; 'E', '191-277' <RES>
 A:Cross-references: EMBL:U26943; NID:g857568; PDB:AA74929.1; PID:g857569
 C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 10.2%; Score 183.5; DB 2; Length 277;
 Best Local Similarity 26.4%; Pred. No. 1.2e-06;
 Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

QY 98 LKDPNNPREEPVX-----KSIOESAFIPQSIPEERYKMKSPKIGICLIID----- 144
 DB 1 MENTENSVSQSKSLNLEPFIHSGSSMDSGLSDSYKMDYPEMGICITITNNKPKHSTG 60
 QY 145 --CIGNETEL--LRDFTSLGVEYQKFLHSMHGISOILGQFACMPEHRDYDSFVCVLV 199
 DB 61 MTRSGTDVDAKLETETMNLKYVRNKNIDLREIYELMDVS-KEDHKSRSFVCVL 119
 QY 200 SRSQSQVYGVDTHTSGPLHHIRRMFGDSCPYLAGKPKFFITQ--NYVSDGQLEDSS 257
 DB 120 SHEEEGIIIG---TNGPVDLKKLTISYFRGDRCRSLTGKPKLFIIOACRGTELDGIEITDS 176
 QY 258 LLEVDPAMKNVEFKAQKRGKGLCTVHREADPFWSLCTADMSLLBQSHSSPSLYLQCLSQKLR 317
 DB 177 GVDDWACHK-----IPEADPLVAYSTAPGYYSWRNKSQSWFIQSLCSMLK 223
 QY 318 RQ 319
 DB 224 KQ 225

RESULT 5
 B54821
 Apoptosis regulator ICH-1, suppressive form S - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C:Accession: B54821
 R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 78, 739-750, 1994
 A:Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulat
 A:Reference number: A54821; MUID:94373811; PMID:8087842
 A:Accession: B54821
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-312 <MAN>
 A:Cross-references: GB:U10322

c;date: 03-06-1999 #sequence_level 03-06-1999 #rev_change 00 nov 2000

c;date: 03-06-1999 #sequence_level 03-06-1999 #rev_change 00 nov 2000

c;date: 03-06-1999 #sequence_level 03-06-1999 #rev_change 00 nov 2000

QY 187 EHRDYSPVCVIVSRGSGSVYGVDTHTSGLPLHHRMFMGDS-CPYLAGKPRMFFION 245
Db 118 ---ELGSLV-----GTCESKGLDSKHSATPIEIVKRAAOKYSVIAVMGKTD----- 162
QY 246 YVSPDQULEDSLSLEVDG-----PAMKVEFFKAQKRG-----LCTVHRB 284
Db 163 -YVSDGK---KVLSTGTGSEYLAITGAGCLHAAACASFSLSKDPLDSMWQLCAFYKQ 217
QY 285 ADFEWSICTADWSLIEOSHSSPSL---YLQCLSQKLRQERGTI 324
Db 218 AAF-----SAOKXALENGSNGSFLFYFLDALSLPIELENSLI 255

Search completed: September 8, 2004, 06:35:41
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 06:05:07 ; Search time 25 Seconds
(without alignments)
724.817 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLPKSDVSLIFLM.....ITKXDMFSSIGCTILDVL 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues
Total number of hits satisfying chosen parameters: 83046

Minimum DB seq length: 0
Maximum DB seq length: 348

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	11.1	293	1	ICB6_HUMAN
2	188.5	10.5	277	1	P55212 homo sapien
3	185.5	10.3	277	1	P70677 mus musculus
4	185.5	10.3	282	1	P55613 rattus norv
5	183.5	10.2	277	1	P55666 xenopus lae
6	183.5	10.2	277	1	O60431 cricetulus
7	172.5	9.6	276	1	P42574 homo sapien
8	167.5	9.3	303	1	ICB6_MOUSE
9	167.5	9.3	312	1	ICB2_RAT
10	163.5	9.1	303	1	ICB2_HUMAN
11	162.5	9.0	303	1	ICB7_MOUSE
12	150	8.3	333	1	ICB7_MESAU
13	149.5	8.3	333	1	ICB7_MOUSE
14	142.5	7.9	299	1	ICB1_SPOFR
15	122	6.8	241	1	ICB1_SPOFR
16	94.5	5.2	344	1	FLIG_BORBU
17	91.5	5.1	216	1	P52810 molluscum c
18	91.5	5.1	248	1	O81173 bacillus ce
19	91.5	5.1	248	1	O8mna4 echinococcu
20	91.5	5.1	248	1	O8mna7 echinococcu
21	89.5	5.0	257	1	ICB6_MOUSE
22	88.5	4.9	184	1	O57823 mus musculu
23	88.5	4.9	168	1	Y099_PYRHO
24	86.5	4.8	208	1	Y099_PYRHO
25	86.5	4.8	208	1	Y099_PYRHO
26	85.5	4.8	209	1	Y099_PYRHO
27	85.5	4.8	209	1	Y099_PYRHO
28	84	4.7	217	1	Y099_PYRHO
29	83.5	4.6	301	1	Y388_AOUAR
30	82.5	4.6	216	1	Y388_AOUAR
31	82	4.6	206	1	UPP_MYCCE
32	82	4.6	255	1	HEA2_AANVA
33	81.5	4.5	252	1	HEA2_AANVA

34	81.5	4.5	280	1	BCCP_ARATH
35	80.5	4.5	171	1	CFIA_HSV2
36	80.5	4.5	242	1	ICB6_HUMAN
37	80.5	4.5	242	1	ICB6_HUMAN
38	80	4.4	244	1	ICB6_HUMAN
39	80	4.4	244	1	ICB6_HUMAN
40	79.5	4.4	184	1	Y099_PYRHO
41	79.5	4.4	184	1	Y099_PYRHO
42	79	4.4	197	1	TRPG_METJA
43	79	4.4	205	1	PADD_MOUSE
44	79	4.4	308	1	Y815_METJA
45	78.5	4.4	214	1	RSS_SULSO

ALIGNMENTS

RESULT 1
ICB6_HUMAN STANDARD; PRT; 293 AA.
ID ICB6_HUMAN
AC P55212; Q9BOE7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6 CR MCH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=95316841; PubMed=7796396;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene family".
RL Cancer Res. 55:2737-2742(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Wiltz L.A., Nickerson D.A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapietson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gnarraire P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grummond J., Schmitt J., Myers R.M.,
RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smalish D.E.,
RA Schmeck A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROCESSING.
RC TISSUE=Lymphocytes;
RX MEDLINE=97059171; PubMed=8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,

```

RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3-interleukin 1beta converting enzyme-like homolog Mch6 and
RT the lamin-leaving enzyme Mcm2alpha are substrates for the apoptotic
RT mediator CPP32.";
RL J. Biol. Chem. 271:27099-27106(1996).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death.
CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=P55212-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P55212-2; Sequence=VSP_000605;
CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNTS.
CC -1- SIMILARITY: Belongs to peptidase family C14.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outpost at
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CC or send an email to license@isb-sib.ch).
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DR EMBL; U20536; AAC50168.1; -.
DR EMBL; U20537; AACS0169.1; -.
DR EMBL; AY254046; AAOC6494.1; -.
DR EMBL; BC000305; AAAH00305.1; -.
DR EMBL; BC004460; AAH04460.1; -.
DR HSSP; P42574; IPRU..
DR MEROPS; C1A.009; -.
DR GeneW; HGNC:1507; CASP6.
DR MIM; 601532; -.
DR GO; GO:0008234; P:cysteine-type peptidase activity; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPRO02138; ICE_p10.
DR InterPro; IPRO01398; ICE_P20.
DR InterPro; IPRO02398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBCENZYM.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS01122; CASPASE_HIS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PSS0207; CASPASE_P10; 1.
DR PROSITE; PSS0208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing;
KW Polymorphism.
FT PROPEP 1 23
FT CHAIN 24 179 CASPASE-6 SUBUNIT p18.
FT PROPEP 180 193
FT CHAIN 194 293 CASPASE-6 SUBUNIT p11.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARY.
FT VARSELIC 14 102 Missing (in isoform Beta).
FT FT 109 /FtID=VSP_000805.
FT VARIANT 109 109 A-> T (in dbSNP:5030674).
FT CONFLICT 66 66 G-> R (IN REF. 1).
SQ SEQUENCE 293 AA; 33310 MW; 073BAEF9791EBD7 CRC64;
Query Match 11.1%; Score 199; DB 1; Length 293;
Best Local Similarity 27.5%; Pred.No.8.ee-06;
Matches 69; Conservative 33; Mismatches 75; Indels 74; Gaps 10.
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16 ENNTETDPAFKREMFDPAEKYMCHRRRRIALIFNHRFFFWLTLPERGTCADBN--
Cy 153 LRDFTSLGAEVQK-----LHLSMGISQIIGFACNCEHRDSDSPCYLVNRSQ 20
Db 74 LTRRSDIGAEVCECFNDLKAEBLLKIHVSTV-----SHADACVCFVLSHGBN 12
Cy 206 SVYGD-----QTHSGPLPH:RRMPMGDSCPYLAKRPFQ-----NYV 24
Db 126 HIYAVDAKIEIQLTLGI-----FKDKCHSLVGRKPIFIIOACRGNDHPVPILDV 17
Cy 249 SDQGL---DSLELVGPMKVERKAKRGCLCYHREAPFPLSLCPLDKMSLLEQSHSP 30
Db 178 VDNQTEKLDNITEVDAAS-----VTLPAADPLMVCYSAEGYSHRETVNG 22
Cy 307 SLVYGLCSOKL 317
Db 226 SWYTDLCENL 236

RESULT 2
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ID ICE3_MOUSE STANDARD: PRT; 277 AA.
AC P706T7.008669:Q9OMI4.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (ICP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE).
CN CASP3 OR CPP32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McEhee I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3."
RT Oncogene 13:749-755(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070890;
RA Mukaa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF."
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
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RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
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RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [12]
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RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [13]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [14]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
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RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [15]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
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RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [16]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
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RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [17]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [18]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [19]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [20]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
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RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [21]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [22]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [23]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
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RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
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RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [26]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [27]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [28]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [29]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [30]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [31]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [32]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandnabeel P., Declercq W., van den Brande I.,
RA van Looy G., Molenaers F., Schotte P., van Crielinge W., Beyers R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RN [33]
RP SE
```

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepiatow M., Soares M.B., Bonaldi M.F., Casavert T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralath P.H.,
 RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Helton E., Ketterman M., Madan A., Rodighiero S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherbenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywiński M.I., Skalska U., Smailus D.E.,
 RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN (6)
 RN SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RT "Multiple pathways of apoptosis converging on the CPP32 protease";
 RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in spleen, liver,
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.
 CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
 CC EMBL: U54803; AAC52768.1; -;
 CC EMBL: U54802; AAC52768.1; JOINED.
 CC EMBL: U49929; AAC52764.1; -;
 CC EMBL: D66352; BAA21727.1; -;
 CC EMBL: Y13086; CAJ73528.1; -;
 CC EMBL: U19522; AAC53196.1; -;
 CC EMBL: BC038825; AAH38825.2; -;
 CC EMBL: U63720; AAD09504.1; -;
 CC PIR: JCS410; JCS410.
 CC HSSP: P42574; 1PAU.
 CC MEROPS: C14.003; -;
 CC MGD; MGI:107739; Casp3.
 CC InterPro: IPR002136; ICE_P10.
 CC InterPro: IPR001309; ICE_P20.
 CC InterPro: IPR002398; Peptidase C14.
 CC Pfam: PF00656; Peptidase C14; 1.
 CC PRINTS: PR00376; IL1BENZME.
 CC SMART: SMO0115; CASC; 1.
 CC PROSITE: PS01122; CASPASE_C15; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 DR

DR PROSITE: PS01207; CASPASE_P10; 1.
 DR PROSITE: PS01208; CASPASE_P20; 1.
 DR Hydroxylase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT PROPEP 10 28 BY SIMILARITY.
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 131 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT CONFLICT 17 17 E -> G (IN REF. 2).
 FT CONFLICT 51 51 N -> T (IN REF. 2).
 FT CONFLICT 63 63 SRS -> ARN (IN REF. 6).
 FT CONFLICT 84 84 Q -> E (IN REF. 2).
 FT CONFLICT 95 95 D -> E (IN REF. 2).
 FT CONFLICT 97 97 L -> M (IN REF. 2).
 FT CONFLICT 128 128 Y -> F (IN REF. 2).
 FT CONFLICT 135 135 E -> D (IN REF. 2).
 FT CONFLICT 231 231 E -> Q (IN REF. 6).
 FT CONFLICT 262 262 I -> F (IN REF. 6).
 SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;
 Query Match 10.5%; Score 188.5; DB 1; Length 277;
 Best Local Similarity 28.9%; Pred. No. Se-07; 92; Indels 37; Gaps 11;
 Matches 67; Conservative 36; Mismatches 92; Indels 37; Gaps 11;
 QY 103 NNRREPPV--KKSIOSEAFPLQSIPEERYKXKPLGICLID-----CTGN 148
 Db 14 NREVTIKGSKSV--DSGIYLDSS-----YKMDYEMGICIIINNKPHKSTGMSSRGCT 67
 QY 149 EFTL--LRPTFSLGCVYQKFLHSMHGSQLGQFACKPEHRDVSVCYLVSQSGSS 206
 Db 68 DVAAALRTFTFGLKQYQVKNKDLREDLELMDVS--KEDSKSSSVCVILSHGDEGV 126
 QY 207 VVGVDQTHSGPLPHIRFMFMGDCPYLAGKPKMFIONVYVSDQLBDSILLEYDGPAM 266
 Db 127 IYV---TNGPVHKLKTLTFRRDGYCRSLGKPKLFIQ---ACRGTELDGC-LEIDSGT- 178
 QY 267 KNYEFAQKRGCLCTVREADFWSLCTADMSLLEQSHSPSYLQCSQKX 318
 Db 179 -DEWACQK-----IPVEDFLYAVSTAGVYSWNSKDGSWFIQSLCSMK 224
 RESULT 3
 ICE3_RAT STANDARD; PRT; 277 AA.
 AC P55213; P70543; P97699; Q62933;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (Casp-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 OS CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761236;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CBD-3.";
 RL Oncogene 13:749-755 (1996).
 RN [2]
 RN SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
 RA Hirstfield A.N., Tilly U.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and

```

CC FT CONFLICT 25 29 C-KMS -> QVD (IN REF. 4) .
CC FT CONFLICT 170 170 C->S (IN REF. 2) .
CC FT CONFLICT 178 178 T->A (IN REF. 2) .
CC FT CONFLICT 182 182 M->V (IN REF. 2) .
CC FT CONFLICT 187 187 I->X (IN REF. 2) .
CC FT CONFLICT 190 190 E->G (IN REF. 3) .
CC FT CONFLICT 199 199 T->S (IN REF. 2) .
CC FT CONFLICT 211 211 D->G (IN REF. 2) .
CC FT CONFLICT 236 236 L->I (IN REF. 4) .
CC FT CONFLICT 245 245 T->M (IN REF. 3) .
CC SQ SEQUENCE 277 AA, 31491 MM, ADAB418E2507402 CRC64;

Query Match 10.3%, Score 185.5; DB 1; Length 277;
Best Local Similarity 27.5%; Pred. No. 8.3e-07;
Matches 64; Conservative 37; Mismatches 93; Indels 39; Gaps 8;

QY 103 NNPREPAPKKS-IQSEAFPLQSIPEHRVKNKSKPLGICLIID-----CIGNPTE 151
DB 14 NNFFTTTHGSKMSDSCGYLDS-----YMDYPEMGDLIINNKNFHKSTGMAKNRTD 68
QY 152 L-----LRDFTSLGAYEQKPLHLSMHSISQLQCFACMEPRHDYDSFYCVLVSRGSGSV 207
DB 69 VDAANLRETFPMALKYEVANKNDLFRREIMELMDSV-KEDHSKRSPFVILSHGDEGVI 127
QY 208 YGVQDTHSGPLPHHRRKFMGDSCEPYLAGKPKKFFIQ--NYVSDQGLDSSLLLEVDSPA 265
DB 128 FG---TNGPVDLKKLTSEFRDDYCRSLTGPKFLIIQACRGTELCGILETSDGDDDMAC 184
QY 266 MNKVFKAQKQKGLCTVREADFPMSLCTADAMSLDEQSHSPSLVQCLISQKLR 318
DB 185 QR-----IPVEADFLVATYATAGYVSMNNSDGSWFIQSLCAWLK 224

RESULT 4
ICE3_XENLA
ID _ICE3_XENLA STANDARD; PRT; 282 AA.
AC PS5866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis precursor (NC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3)
DE (CASP-3) (XCPP32) .
GN CASP3.
OS Xenopus laevis (African clawed frog) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RX MEDLINE=97184166; PubMed=9030578;
RP SEQUENCE FROM N.A.
RA Yodaïta Y., Nakajima K.,
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
RT myoblastic cell line derived from tadpole tail";
RL J. Biol. Chem. 272:5122-5127(1997) .
CC -I- FUNCTION: Important mediator of apoptosis. At the onset of
CC apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase
CC (PARP) at a 216-Asp-Gly-217 bond (By similarity) .
CC -I- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12)
CC subunits.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity) .
CC -I- MISCELLANEOUS: The subunits are derived from the precursor
CC sequence by a probable autocatalytic mechanism and probably by
CC other caspases (By similarity) .
CC -I- SIMILARITY: Belongs to peptidase family C14.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydroxylase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1
FT CHAIN 186
FT ACT_SITE 187
FT ACT_SITE 131
FT ACT_SITE 174
FT SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;

Query Match 10.3%; Score 185.5; DB 1; Length 282;
Best Local Similarity 29.4%; Pred. No. 8.5e-07;
Matches 63; Conservative 33; Mismatches 71; Indels 47; Gaps 11;

QY 128 ERYKMSKPLGICLID-----CIGNETEL-----LRDFTSLGYEV-----QKFLH 169
DB 46 QNRYRTPPEKMCILINNNKFSNNANVANGVDYALKHEFTGLGYEWVWQNDK--- 102
QY 170 LSMHGISQILGFACMPE--HRDYDFVCVLVSRGSGQ-SYGVQDQHSGLPLH--HRR 224
DB 103 -----SSDITGLRLKISEEDHSKRSFVCAILSHGEDDSIGVD-----VPIHKNLTD 152
QY 225 MFWGDSQPVLAGPKPKFFIGNVYVSGOLEDSLLLEVDPAKNVFFKAKGKGLCTVARE 284
DB 153 LFRDRKRLTVGPKKFFIQ--ACRGTELDSC-ITDSCSPREPIQ-----RIEVE 201
QY 285 ADFEWSLCTADMSLDEQSHSSPSLYOCLSQKLR 318
DB 202 ADFLYAVSTVPGYCSWRDKMDGSMFQISLCKMK 235

RESULT 5
ICE3_CRILLO STANDARD; PRT; 277 AA.
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CpP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1).
DE CASP3 OR CPP32.
DE Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
DE Cricetulus.
OX NCBI_TaxID=10030;
RX MEDLINE=96183165; PubMed=8605870;
RA Wang X., Zelenksi N.G., Yang J., Sakai J., Brown M.S.,
RA Goldstein J.L.;
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis."
RT EMO J. 15:1012-1020(1996).
CC -I- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-

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CC helix leucine zipper domain and the membrane attachment domain.
CC cleaves and activates caspase-6, -7 and -9 (by similarity).
CC -I- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (by similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROPEP. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROPEP AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -I- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U27463; AAB01511.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydroxylase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1
FT CHAIN 10
FT ACT_SITE 28
FT CHAIN 229
FT CHAIN 176
FT ACT_SITE 121
FT ACT_SITE 163
FT SEQUENCE 277 AA; 31612 MW; 0BF3A4590A828A3 CRC64;

Query Match 10.2%; Score 183.5; DB 1; Length 277;
Best Local Similarity 27.9%; Pred. No. 1.2e-06;
Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

QY 96 KSLKDPNNFRPEPVKKS-IQSEAFLLPOSIPERYKKSKPLGICLID----- 144
DB 11 KSLK-----NPEVKTINGSKMSDGYLDS-----YKMDYPMGVCIILINNNFKHSTGM 61
QY 145 --CIGNETEL--LRDFTSLGYEVQKFLHLSMHGISQILGQACMPEHRDYSFVCVAYS 200
DB 62 TPRSQDVVPAAKRLRFPMALKYEVNRKNDLTREELVELM-KVASKEDHSKRSFVCVILS 120
QY 201 RGSQSVYGVQDQHSGLPLPHIRFMFMGDSCPYLAGKPKMFFIQ--NVVPSDQLEDSSL 258
DB 121 HDDEGVIFGID--GPIDLKULTSYFRGDYCRSLGKPLFLIQACRGTELDGCIETDSG 177
QY 259 LEVDGPKMKNVEFKAKRGKGLCTVHRADFFMSLCTADNSLDEQSHSSPSLYOCLSQKLR 318
DB 178 TEDDMTCQK-----IPVEDPLVAVSTAPGYYSWRNPKDGSWMFQISLCSMLK 224

RESULT 6
ICE3_HUMAN STANDARD; PRT; 277 AA.
AC P42574; Q96AN1; Q96KP2;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CpP-32) (Caspase-3) (SREBP cleavage activity 1)

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DE (SCA-1).
GN CASP3 OR CPP32.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=T-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3, is a CrmA-inhibitable
RT interleukin-1 beta-converting enzyme.";
RL J. Biol. Chem. 269:30761-30764 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnecys S., Zeng Z.,
RA Beutler D.R., Poitrier G.G., Salvesen G.S., Dixit V.M.;
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Vallette F.M., Oliver L.J.;
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schickwitz W.S., Sherwood J.K., Wittek L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Mearns K., Farmer A.A., Rubin G.M., Hong L.,
RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzyzanski M.I., Skalka U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
RX MEDLINE=95315529; PubMed=7596430;
RA Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
RA Gallant M., Gareau Y., Griffen P.R., Labelle M., Lezbeik Y.A.,
RA Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
RA Miller D.K.;
RT "Identification and inhibition of the ICE/CED-3 protease necessary
RT for mammalian apoptosis.";
RL Nature 376:37-43 (1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=96266352; PubMed=8673606;

RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
RA Thornberry N.A., Becker J.W.;
RT "The three-dimensional structure of apopain/CPP32, a key mediator of
RT apoptosis.";
RL Nat. Struct. Biol. 3:619-625 (1996).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RX MEDLINE=97197830; PubMed=9045680;
RA Mitzi P.R.E., di Marco S., Krebs J.F., Bai X., Karnewsky D.S.,
RA Picot J.P., Tomasselli K.D., Grutler M.G.;
RT "Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RL J. Biol. Chem. 272:6539-6547 (1997).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20283632; PubMed=10821855;
RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
RA Levy M.A., Demolfi W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
RA Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RT inhibit apoptosis and maintain cell functionality.";
RL J. Biol. Chem. 275:16007-16014 (2000).
RN [10]
RP PROCESSING.
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomasselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FAD2-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
RN [11]
RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vaillancourt J.P., Hayden M.R.;
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449 (1996).
RN [12]
RP FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-|-Gly-217 bond. Cleaves and activates steroid regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9. Involved in the
CC cleavage of huntingtin.
CC -1- ENZYME REGULATION: Inhibited by isatin sulfonamides.
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC -1- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC EMBL; U13737; AAA65015.1; -
DR EMBL; U13738; AAA60355.1; -
DR EMBL; U26943; AAA74929.1; -
DR EMBL; A013269; CAC08866.1; -
DR EMBL; A219866; AA025654.1; -
DR EMBL; BC016926; AAH16926.1; -
DR PIR; A55315; A55315.
DR PDB; 1PAU; 07-JUL-97.
DR PDB; 1CP3; 24-DEC-97.
DR PDB; 1GFW; 23-JUN-00.
DR MEROPS; C14.003; -
DR Genew; HGNC:1504; CASP3.
DR MIM; 600636; -
DR GO; GO:0004208; F:caspase-3 activity; TAS.
DR GO; GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
DR GO; GO:0008629; P:induction of apoptosis by intracellular sig. .; TAS.
DR GO; GO:0009405; P:apoptogenesis; TAS.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01123; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT VARIANT 190 190
FT CONFLICT 31 36
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT TURN 67 80
FT HELIX 81 82
TURN 82

Query Match 10.2%; Score 183.5; DB 1; Length 277;
Best Local Similarity 26.4%; Pred. No. 1.2e-06;
Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

CC EMBL; Y13087; CAA73529.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.005; -
DR MGD; MGI:1312921; Casp6.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 5
FT CHAIN 6 162
FT PROPEP 163 176
FT CHAIN 177 276
FT ACT_SITE 104 104
FT ACT_SITE 146 146
SEQUENCE 276 AA; 31595 MW; 59650E9321126B6C CRC64;

Query Match 9.6%; Score 172.5; DB 1; Length 276;
Best Local Similarity 27.8%; Pred. No. 7.7e-06;
Matches 62; Conservative 26; Mismatches 84; Indels 51; Gaps 8;

RESULT 7
ICE6_MOUSE
ID ICE6_MOUSE STANDARD; PRT; 276 AA.
AC 008738;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN Casp6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen W., Vandenaebroeck P., Declercq W., van den Brande I.,
RA van Leeuwen G., Molemans F., Schotte P., van Crieginge W., Beyaert R.,
RA Piers W.;
RT "Characterization of seven murine caspase family members."
RL FEBS Lett. 403:61-69(1997).
CC - FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death (By similarity).
CC - SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
CC (By similarity).
CC - SUBCELLULAR LOCATION: Cytoplasmic.
CC - TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
CC testis, and heart. Lower levels in spleen, skeletal muscle and
CC brain.
CC - PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS (BY SIMILARITY).
CC - SIMILARITY: Belongs to peptidase family C14.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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CC
CC EMBL; Y13087; CAA73529.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.005; -
DR MGD; MGI:1312921; Casp6.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 5
FT CHAIN 6 162
FT PROPEP 163 176
FT CHAIN 177 276
FT ACT_SITE 104 104
FT ACT_SITE 146 146
SEQUENCE 276 AA; 31595 MW; 59650E9321126B6C CRC64;

Query Match 9.6%; Score 172.5; DB 1; Length 276;
Best Local Similarity 27.8%; Pred. No. 7.7e-06;
Matches 62; Conservative 26; Mismatches 84; Indels 51; Gaps 8;

Db 16 PAEQYMDHRRGVALIFNEHRRFWHLTPERRGTNADRLTRFSDLGFEVCKFNDLR 75
 Qy 168 ---LHLSMGISQILGQFACMEHEDYDPSFVCVLVSRRGSGSYGVG-----CHSGPL 219
 Db 76 AEELLKIHVE-----TSHLDACCFICVLSHGGNVAIYAKIIEIQTGL-- 125
 Qy 220 HHIREWMDSCPYLAGKPKMEFFIONVYVSGQEDSSILEVD-----GPAKMEFFKAQ 274
 Db 126 -----FKGDKCQSQVXKPKFIIO---ACRGSQHDVVPVPLDWVHDQTKLDNVT-QVD 175
 Qy 275 KXGLCTVREADPFWSLCTADWSLLEQSHSPSLYLQCTSKL 317
 Db 176 AASVTLTPAGADFLMCVYASGYSHRETVGSMYIDLCBML 218

RESULT 8
 ICE7 HUMAN STANDARD: PRT: 303 AA.
 AC P55210; Q13364; Q96B80;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMT-1).
 GN CASP7 OR MCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=96139498; PubMed=8576161;
 RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
 RA Dixit V.M.,
 RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
 RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
 RT factor-induced apoptosis.";
 RL J. Biol. Chem. 271:1621-1625(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX TISSUE=Spleen;
 RX MEDLINE=96147144; PubMed=8567622;
 RA Lipke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.,
 RA "Identification and characterization of CPP32/Mch2 homolog 1, a novel
 RT cysteine protease similar to CPP32.";
 RL J. Biol. Chem. 271:1825-1828(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX TISSUE=T-cell;
 RX MEDLINE=96105019; PubMed=8523391;
 RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
 RA Fritz L.C., Tomasselli K.J., Wang L., Yu Z., Croce C.M., Salvenson G.,
 RA Barnshaw W.C., Litwack G., Alnemri E.S.,
 RT "Mch3, a novel human apoptotic cysteine protease highly related to
 RT CPP32.";
 RL Cancer Res. 55:6045-6052(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
 RX TISSUE=Fetal lung, and Fetal spleen;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher P.A.,
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX TISSUE=Skin;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fabley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PROCESSING.
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomasselli K.J.,
 RA Litwack G., Alnemri E.S.,
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADd-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Cleaves and activates sterol
 CC regulatory element binding proteins (SREBPs). Proteolytically
 CC cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
 CC bond. Overexpression promotes programmed cell death.
 CC -1- ENZYME REGULATION: Inhibited by Icatin sulfonamides.
 CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=Alpha;
 CC IsoId=P55210-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=P55210-2; Sequence=VSP_000807;
 CC Note=Not proteolytically active;
 CC Name=Alpha'; Synonyms=Beta;
 CC IsoId=P55210-3; Sequence=VSP_000806;
 CC Note=What we call isoform Alpha' is known in Ref.4 as Beta;
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung, skeletal muscle,
 CC liver, kidney, spleen and heart, and moderately in testis. No
 CC expression in the brain.
 CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC EMBL; U93613; AAC50346.1; -;
 CC EMBL; U40281; AAC50352.1; -;
 CC EMBL; U37448; AAC50303.1; -;
 CC EMBL; U37449; AAC50304.1; -;
 CC EMBL; U67319; AAC51152.1; -;
 CC EMBL; U67320; AAC51153.1; -;
 CC EMBL; U67206; AAF21460.1; -;
 CC EMBL; BC015799; AAF15799.1; -;
 CC PDB; 1FJ1; 23-MAY-01.
 CC PDB; 1IGF; 04-JAN-02.
 CC PDB; 1I40; 31-OCT-01.
 CC PDB; 1I51; 23-FEB-02.

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DR PDB; 1K86; 21-NOV-01.
DR PDB; 1K88; 21-NOV-01.
DR PDB; 1KMC; 16-JAN-02.
DR MEROPS; C14.004; -.
DR Genem; HGNC:1508; CASP7.
DR MIM; 601761; -.
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0008234; Fcysteine-type peptidase activity; TAS.
DR GO; GO:0008632; Piapoptotic program; TAS.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW 3D-structure.
FT PROPEP 1 23
FT CHAIN 24 198
FT PROPEP 206
FT CHAIN 207 303
FT ACT_SITE 144 144
FT ACT_SITE 186 186
FT VARSPLIC 1 1
FT VARSPLIC 149 303
FT VARSPLIC 303 AA; 34276 MM; CD373EE54A232CA4 CRC64;
MUTAGEN 186 186
FT CONFLICT 194 194
FT CONFLICT 194 194
FT SEQUENCE 303 AA; 34276 MM; CD373EE54A232CA4 CRC64;
Query Match 9.3%; Score 167.5; DB 1; Length 303;
Best Local Similarity 22.4%; Pred. No. 2, 1e-05;
Matches 69; Conservative 43; Mismatches 119; Indels 77; Gaps 11;
98 LKPSNNPREPPVKSIQES-----EAFLP-----QSIPEERY 130
1 MADDOGCIIEGGVEDSANEDSVDAKPDSSFPVSLPSKKKXVYRSIKTRDRVFTYQY 60
131 KKKSKPIGICLI-----DCIGNETELIDFTSLGYEVOKFLHLSWGIS 176
61 NMNFEKLGKCTIINNKNPKDKYTGNGVANGDKDAEALFKCFRSLGFDIVYNDSCAKMQ 120
177 QILQFACMPHRDYDFVLCVLSRGSGQVYGVDTGSLPLHIRRMWGDSCPYLAG 236
121 DLTKK-ASEEDHTNAACFACILSHGEEVNIYGDGV--TPIKDLTAHFRGRCKTLLE 176
237 KKKKFFIACGCTELDDGIQADSGPINDTA---NPRK-----IPVEDLPAIS 224
233 TADMSLEQSHSPSLYLQCLQKLRQERGTIPSGI-----TESKDNHF-- 337
225 TVPGYYSRSGRSGWFWQALCSILEHGKDLIMQLTRVNDVARHFEQSDDPHFHE 284
338 -SSLGCTL 344
285 KKQIPCV 292

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ICE2 RAT
ID ICE2 RAT STANDARD; PRT; 312 AA.
AC PS215; 035398;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease)
DE (Fragment)
DE CASP2 OR ICH1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE OF 1-257 FROM N.A.
RC TISSUE=Kidney cortex;
RA MEDLINE=98191309; PubMed=9530276;
RA Kausel G.P., Singh A.B., Shah S.V.;
RT "Identification of gene family of caspases in rat kidney and altered
RT expression in ischemia-reperfusion injury.";
RL Am. J. Physiol. 274:F587-F595(1998).
RN [2]
RP SEQUENCE OF 131-312 FROM N.A.
RC TISSUE=Ovary;
RA MEDLINE=96042508; PubMed=7588240;
RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
RA Hirschfield A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle.";
RL Endocrinology 136:5042-5053(1995).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival (By similarity).
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
DR EMBL; AF025671; AAB82567.1; -.
DR EMBL; U34684; AAC52260.1; -.
DR PIR; I67436; I67436.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.006; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
KW HydroLase; Thiol protease; Apoptosis; Zymogen.
FT NON_TER 1
FT CHAIN <1 266
FT CHAIN 267 >312
FT CHAIN 281 >312
CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
CASPASE-2 SUBUNIT P12 (BY SIMILARITY).

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RESULT 9

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FT DOMAIN <1 55 CARD.
FT ACT_SITE 210 210 BY SIMILARITY.
FT ACT_SITE 253 253 BY SIMILARITY.
FT NON_TER 312 312
SQ SEQUENCE 312 AA; 35070 MW; 318A0746212B3646 CRC64;

Query Match 9.3%; Score 167.5; DB 1; Length 312;
Best Local Similarity 31.1%; Pred. No. 2.1e-05;
Matches 46; Conservative 22; Mismatches 61; Indels 19; Gaps 4;

QY 130 YMKSKPGICILIDCI-----GNBTE--LIRDFTSLGVEYQKFLHLSMGI 175
DB 125 YKQSPKRLALVMSNVHFTGKLEFRSGDVTHTLVTLFKLGYNVHLYDQRAQEN 184
QY 176 SOLIQFACMPHEDYDSFVCVLVSRGSGSVGVQDTHSGLPPLHIRMFGDSCPYL 235
DB 185 QEKQNFAGLPAHRTVDSQVALSHGVGGIYGD--GKLLQQLGVFRLEPDANCPSLQ 242
QY 236 GPKKPFQNTVSVSGQLBDSLLFVDG 263
DB 243 NKPKMFFIQ--ACRGDETDGVDQDG 267

RESULT 10
ICE7 MOUSE STANDARD; PRT; 303 AA.
AC P97864; 008669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
GN Casp7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argente J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher P.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genomics 40:66-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Mortamun enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid."
RL Biochem. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaabee P., Declercq W., van den Brande T.,
RA van Looy G., Molemans F., Schotte P., van Clikinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dalcenno L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

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Db      6 DCAAELEKVDSSSEDDVDKPPDRSSITSSILLKKK----- 40
Qy      97 SLKDPNNFEEEPVKKSIOESEAFLPQSIPEERRYMKSKPLGICLITD-----CI 146
Db      41 -----RMSAGVFRGT-----RDRVPTLYLRMDPCKMKKCIILNNKPKATGNDV 86
Qy      147 GNETE-----LLRDTFSLGVEVKFLHLSMHGISQLGQFACMPHRYDSEFVCVYLRG 202
Db      87 RNTGTDADAGLFFCFQNLGFVYVNHDCSCAKMDLLRK-ASEERHNSACFACVLSHG 145
Qy      203 GSGSVYGVDPDTHSGPLHRIIRFMFGDSCPYLAGKPKMFIONVYVSDGQLEDSSLEVD 262
Db      146 EEDLYGKDGVV---TPIKDLTAHFRDGRCKTLLEKXLFPIQ--ACRGTELDG--IQAD 198
Qy      263 GPMKVVPEFAKRGGLCTVAREDFMSLCTDMSLLEQSHSPSLYLCCLSQKLRQ 319
Db      199 SGPTINDIDANPRNK---IPVEADFLFAYSTVPGYVSWNPKGSMFVQALCSITLNE 251

RESULT 11
ICE7_MESAU STANDARD; PRT; 303 AA.
AC P55214;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
Caasase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (SRBP cleavage activity 2)
DE (SCA-2).
DE CASP7 OR MCH3.
OS Mesocricetus auratus (Golden hamster).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=Syrian; TISSUE=Liver;
RX MEDLINE=96224303; PubMed=864593;
RX Pal J.-T., Brown M.S., Goldstein J.L.;
RX "Purification and cDNA cloning of a second apoptosis-related cysteine
protease that cleaves and activates sterol regulatory element binding
proteins."; Acad. Sci. U.S.A. 93:5437-5442(1996).
RT proc. Natl.
RI -1- FUNCTION: Involved in the activation cascade of caspases
responsibile for apoptosis execution. Cleaves and activates sterol
regulatory element binding proteins (SRBPs). Proteolytically
cleaves poly(ADP-ribose) polymerase (PARP) at a 216-ASP-Gly-217
bond. Overexpression promotes programmed cell death (by
similarity).
CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
(BY similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGES BY GRAZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CPR32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CASPASE-7 AND THE LARGE SUBUNIT OF CPR32 PROTEASE ALSO OCCUR AND
VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
CC EMBL: U47332; AAC52595.1; -.
CC HGSB; P42574; 1PNU.
CC MEROPS; C14.004; -.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.

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DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PR00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIHCENZME.
DR SMART; SM00115; CASc_1.
DR PROSITE; PS01122; CASPASE_CYS_1.
DR PROSITE; PS01121; CASPASE_HIS_1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT SITE 144 144 BY SIMILARITY.
FT ACT SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match 9.0%; Score 162.5; DB 1; Length 303;
Best Local Similarity 26.9%; Pred. No. 4,9e-05;
Matches 58; Conservative 31; Mismatches 92; Indels 35; Gaps 8;

Qy 125 IPEERYMKSKPLGICLIT-----DCIGNETELLRDTFSLGVEVKFLHL 170
Db 55 VPTVLYRMDFEKKKCIILNNKPNFKYGMVNRNGTDAEALFKCFRSLGPDVYVYVDC 114
Qy 171 SMHGISQLGQFACMPHERDYDSFVCVLYSRGSGSVYGVDPDTHSGPLHRIIRFMFGDS 230
Db 115 SCARKMDLLRK-ASEERHNSACFACVLSHGENTLYGKGV---TPIKDLTAHFRDR 170
Qy 231 CPYLAKPKMFFIQ--NVVSDG--CLEDSLSLEVGPAMKVEFAKRGGLCTVHRAD 286
Db 171 CKTLLEKPLFFIQACRGTELDGVQADSGPINEIDA-----NPRVK-----IPVEAD 218
Qy 287 FFWSLCTADMSLLEQSHSPSLYLCCLSQKLRQERG 322
Db 219 FLFAYSTVPGYVSWNPKGSMFVQALCSITL-DEHG 253

RESULT 12
ICE1_DROME STANDARD; PRT; 323 AA.
AC 002032; Q9WIN0;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-).
DE DCP-1 OR CG5370.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.
RX TISSUE=Embryo;
RX MEDLINE=20196006; PubMed=8999799;
RX Song Z., McCall K., Steller H.;
RX "DCP-1, a Drosophila cell death protease essential for development.";
RT Science 273:536-540(1997).
RL Science 273:536-540(1997).
RN [2]
RP ERRATUM.
RX Song Z., McCall K., Steller H.;
RL Science 277:167-167(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RX MEDLINE=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RX Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RX Sutton G.G., Wortman J.R., Vandell M.D., Zhang O., Chen L.X.,
RX Brandon R.C., Rogers Y.-H.C., Blazer J.R.G., Chame M., Pfeiffer B.D.,
RX Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

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RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Bouchan M.R., Bouck U., Brokstein P., Brothier C.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gloske A., Gong F., Gorrell T.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison U.A., Ketchum K.A.,
RA Kimmel B.E., Kodra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshell A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spiedling A.C., Stapleton M., Strong R., Sun E.,
RA Switzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massaman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zhang X.H., Zhong F.N., Zhong S., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.",
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Embryo;
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.W.,
RA Chape M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
RA Miranda A., Mungai C.J., Nuno J., Pacleb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.E.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution (By similarity). (PARP). Loss
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP). Loss
CC of zygotic DCP-1 function causes larval lethality and melanotic
CC tumors.
CC -1- SUBUNIT: Heterodimer of a 22 kDa (p22) and a 13 kDa (p13) subunit.
CC -1- DEVELOPMENTAL STAGE: Present uniformly throughout embryos of
CC stages 4 and 10. In stage 16 embryos, the expression becomes
CC restricted to the central nervous system, the developing gonads,
CC and a portion of the gut. In stage 17 embryos, expression is
CC mainly localized in cells along the midline of the central nervous
CC system.
CC -1- SIMILARITY: Belongs to peptidase family C14.
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CC -----
DR EMBL: AF001464; AAB58237.1; -
DR EMBL: AE003461; AAF47027.1; -
DR EMBL: BT010065; AAQ2534.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.016; -
DR FLYBase: FBgn0010501; Dcp-1.
DR GO: GO:0004159; F:caspase activity; IDA.
DR GO: GO:0004207; F:effector caspase activity; NAS.
DR GO: GO:0030036; P:actin cytoskeleton organization and biogenesis; IMP.

DR GO: GO:0008632; P:apoptotic program; IDA.
DR GO: GO:0008922; P:cleavage of lamin; IMP.
DR GO: GO:0009795; P:embryonic morphogenesis; IMP.
DR GO: GO:0007300; P:nurse cell/occyte transport (sensu insecta); IMP.
DR InterPro: IPR002138; ICE p10.
DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002398; peptidase C14.
DR Pfam: PF00655; peptidase C14; I.
DR PRINTS: PR00376; ILBCENZTME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 33 PROBABLE.
FT CHAIN 34 202 CASPASE-1 SUBUNIT P22.
FT PROPEP 203 215
FT CHAIN 216 323 CASPASE-1 SUBUNIT P13.
FT ACT_SITE 154 154 BY SIMILARITY.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35926 MW; 5BF0F75E8E2BD CRC64;

Query Match 8.3%; Score 150; DB 1; Length 323;
Best Local Similarity 25.2%; Pred. No. 0.00045;
Matches 59; Conservative 37; Mismatches 94; Indels 44; Gaps 9;

OY 101 PNNNF-REEVKKSIDSESEFLQSPERRYMKSKPGICLI-----IDCIGNET-- 150
DB 54 PANKFAKMFVERVYAS-----YNNSHKRCVALIFNHEFFDPSLKSRTGT 100
OY 151 ----ELRDPTSLGYEVQKFLHLSMNGISQILGCFACPEHRDYDSFVCVLVSRGQS 206
DB 101 NVDAQELKKAFENLGFVAVHVKCKRLDKVYKAAEL-DHTDNDCLAVAILSHGNGY 159
OY 207 YGVDQCHSLPLPHHRRNFMGDSCTYLAKRKMPFI---QYVVSQDLBSSLSLEVDG 263
DB 160 LVAKDQYK--LDNIWHYFTATPCPSLGRKPLFFIQACQDRLDGGITTEKGVETDG 216
OY 264 PAKNKVEFKQKRGKGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLOCLSQKL 317
DB 217 EESISYKLT-----PIH--ADFLFSYSTIGFYSPKNNNGSNVYMSGLREL 260

RESULT 13
ID ICE DROME STANDARD; PRT; 339 AA.
AC 001382; Q9VAH1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase precursor (EC 3.4.22.-) (dtcB).
GN ICE OR CG7788.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97327558; PubMed=9184225;
RA Fraser A.G., Evan G.I.;
RT "Identification of a Drosophila melanogaster ICE/CED-3-related
RT protease, dtcB".
RL EMBL J. 16:2805-2813(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Maniatis P.G., Scher S.B., Li P.W., Hoskins R.A., Galie R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner K., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Malow G.L.G.,
 RA Abiri J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.D., Beron F.V., Bernan B.P., Bhandal D., Bolintsov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Butts K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Deltcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwe C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kension J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venler E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkeley; TISSUE=Head;
 RC MEDLINE=22426066; PubMed=12537569;
 RX Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Paclebo J.M., Park S., Wan K.H.,
 RA Rubin G.M., Gelinker S.E.;
 RA "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Acts downstream of rpr.
 CC Cleaves baculovirus p35 and Iamln DMO in vitro.
 CC -!- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
 CC -!- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
 CC occurs.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y12611, CAJ2937.1, -;
 DR EMBL: AE003771, AAF56939.1, -;
 DR EMBL: AY058451, AAL13680.1, -;
 DR HSSP: P42574, 1PAU.
 DR MEROPS: C14.015, -;
 DR FLYBase: FBgn0019972; Ice.
 DR GO: GO:0004207; P:effector caspase activity; NAS.
 DR GO: GO:0006915; P:apoptosis; NAS.
 DR InterPro: IPR001309; ICE_p10.
 DR InterPro: IPR002398; Peptidase C14.
 DR Pfam: PF00656; Peptidase C14; I.
 DR PRINTS: PR00376; ILBCNZME.

DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PSS0207; CASPASE_P10; 1.
 DR PROSITE: PSS0208; CASPASE_P20; 1.
 DR PROSITE: PSS0209; CASPASE_P20; 1.
 DR HYDROLASE; Thiol protease; Zymogen, Apoptosis.
 KM PROPEP 1 28
 FT CHAIN 29 217
 FT PROPEP 218 230
 FT CHAIN 231 339
 FT ACT_SITE 169 169
 FT ACT_SITE 211 211
 FT ACT_SITE 211 211
 FT CONFLICT 151 151
 FT CONFLICT 265 265
 SQ SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;
 Query March 8.3%; Score 149.5; DB 1; Length 339;
 Best Local Similarity 24.2%; Pred. No. 0.00052;
 Matches 63; Conservative 40; Mismatches 108; Indels 49; Gaps 11;
 79 VQAGTSYRNVLQALQKSLKDPNNFRPEPKSIOESEAFLOPISPEERYKMSKPLG 138
 44 VAGSSHPYSGAIGQANGYSSPSRYKN-VAKQVTDHRA-----AEYMHKQKG 94
 139 ICIL-----IDCGNETLRDPTFSLGCVQKPLHSMHGISQLG 180
 95 MALIFHEHEVPTLKSRAQTNVDC-ENLTVLK---QLDEVTYADCRKYDLRTI- 148
 181 QPACMEPHRDYDFVCULVSRGSGSVGVDPQTHSGPLPHIRFRPMGDCPYLAGKPKM 240
 149 EYASQNHSSDDILVAISHGEMGYIAKDIQYK---LDNWSFTFNHCGSLAGKRYL 205
 241 FFI---QNVVSSGQLDEDSLEVDGPANKVFEKQKRGCLCTVAREDFMSLTADWS 297
 206 FFIQACQGRDLQGVGMQSRQETEDGDS--SMSYK-----IPVH-ADFLVASTVDFG 255
 298 LLEQSHSPSLYQCLCSOKL 317
 256 YSRNRTTRGSMFMQSLCAEL 275
 RESULT 14
 ID_CEL_SPOFR STANDARD; PRT; 299 AA.
 AC P891G;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-1 precursor (EC 3.4.22.-).
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Amphipyritinae; Spodoptera.
 OX NCBI_Taxid=7108;
 RN [1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97153084; PubMed=8999805;
 RA Ahmad M., Srinivasula S.M., Wang L., Litwack G., Fernandes-Alnemri T.,
 RA Alnemri E.S.;
 RA "Spodoptera frugiperda caspase-1, a novel insect death protease that
 RT cleaves the nuclear immunophilin FKBP46, is the target of the
 RL baculovirus antiapoptotic protein p35.";
 RL J. Biol. Chem. 272:1421-1424(1997).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution (By similarity). Inhibited by
 CC the baculovirus anti-apoptotic protein p35. Cleaves p35 and
 CC nuclear immunophilin FKBP46.
 CC -!- SUBUNIT: Heterodimer of a 19/18 kDa (p19/18) and a 12 kDa (p12)
 CC subunit.
 CC -!- PM: AN AUTOCATALYTIC MECHANISM GENERATES THE TWO ACTIVE SUBUNITS.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC EMBL; U81510; AAC7442.1; -
 DR HSSP; P42574; 1CP3.
 DR MEROPS; C14.015; -
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; 1LBCENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 28
 FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.
 FT PROPEP 185 195 POTENTIAL.
 FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.
 FT ACT_SITE 136 136 BY SIMILARITY.
 FT ACT_SITE 178 178 BY SIMILARITY.
 SQ SEQUENCE 299 AA; 33527 MW; 99F4FED09B04EEDE CRC64;

 Query Match 7.9%; Score 142.5; DB 1; Length 299;
 Best Local Similarity 24.1%; Pred. No. 0.0015;
 Matches 66; Conservative 37; Mismatches 112; Indels 59; Gaps 12;
 QY 62 NHRDLKTKIOKYSQAGTSYRVVLAALIKSLKDSNNFRPREPKKSGSEARL 121
 DB 10 NVDSDVI-----KQRTNGGDD-----GDALGSSSSQPNVARNPVRN----- 49
 QY 122 PQSIEERYKMKSKELGICLI-----IDCIGNET-----ELLRDTFSLGEYQKFL 168
 DB 50 -----APYNNMHKRGKALIFNHEHDPHSLKRTGTNVDSNLKVLKLGKXTVPR 104
 QY 169 HUSMHGISQILGQFACMPERHDYSPVCVLVSRGSGSVYGVQDTGSLPLHHRPMFG 228
 DB 105 NIKSEINKFIOQTAEK-DHSDDADCLVAVLTHGELMLYAKD-TH--YKPDWLWYFYRA 160
 QY 229 DSCPYLAGKPKKPFQONVVVSDGQLEDS---SLLEVDPAMKQVFKAKQKGLCTVARE 284
 DB 161 DKCPFLAGKPKLFFIQ--ACQGRDLGGITLSTETDSSPSTSYRI-----FVH-- 207
 QY 285 ADFWSLCTADMSILBOGSHSSPSLYLQCLSGKLR 318
 DB 208 ADFLIASFVPGYFSEMTTRGSMFQALCELR 241

 RESULT 15
 CFWL_MCV1 STANDARD; PRT; 241 AA.
 ID CFWL_MCV1 098325; 011298;
 AC 098325; 011298;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Viral CASPase and FADD-like apoptosis regulator (v-CFLAR) (Viral
 DE FLICE-inhibitory protein) (v-FLIP).
 GN 159L OR H-H2.2.
 OS Moluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Moluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]_TaxID=10280;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96325459; PubMed=8670425;
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
 RA Moss B.;

RT "Genome sequence of a human tumorigenic poxvirus: prediction of
 RT specific host response-evasion genes."; Science 273:813-816(1996).
 RL [2]
 RN SEQUENCE OF 91-241 FROM N.A.
 RX MEDLINE=97352177; PubMed=9208457;
 RA Moratilla M., Agronayor M., Nunez A., Funes J.M., Varas A.J.,
 RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.,
 RA "A random DNA sequencing, computer-based approach for the generation
 RT of a gene map of moluscum contagiosum virus."; Virus Genes 14:73-80(1997).
 RN [3]
 RN FUNCTION.
 RP MEDLINE=97242415; PubMed=9087414;
 RX Thome M., Schneider P., Hofmann K., Fickenscher H., Meini E.,
 RA Neipel F., Matlman C., Burns K., Bodmer U., Schrotter M.,
 RA Scalfidi C., Krammer P.H., Peter M.E., Tschopp U.,
 RT "Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by
 RT death receptors."; Nature 386:517-521(1997).
 RL [4]
 RN FUNCTION.
 RP MEDLINE=97188440; PubMed=9037025;
 RX Bertin J., Armstrong R.C., Oltine S., Martin D.A., Wang Y., Banks S.,
 RA Wang G.-H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J.,
 RA Tomaselli K.J., Cohen J.I.,
 RT "Death effector domain-containing herpesvirus and poxvirus proteins
 RT inhibit both Fas- and TNF α -induced apoptosis"; Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).
 RN [5]
 RN CHARACTERIZATION.
 RP MEDLINE=99457304; PubMed=10526240;
 RX Tsukumo S.I., Yonehara S.,
 RA "Requirement of cooperative functions of two repeated death effector
 RT domains in caspase-8 and in MCL1 for induction and inhibition of
 RT apoptosis, respectively."; Genes Cells 4:541-549(1999).
 CC -1- FUNCTION: INHIBITS TNFRSF1A, TNFRSF6 AND TNFRSF12 INDUCED
 CC APOPTOSIS. MAY INTERFERE WITH CASPASE-8 RECRUITMENT AND ACTIVATION
 CC AT THE DEATH-INDUCING SIGNALING COMPLEX (DISC). MAY LEAD TO HIGHER
 CC VIRUS PRODUCTION AND CONTRIBUTE TO VIRUS PERSISTENCE AND
 CC ONCOGENICITY.
 CC -1- SUBUNIT: ASSOCIATES WITH THE DEATH-INDUCING SIGNALING COMPLEX
 CC (DISC) FORMED BY TNFRSF6, FADD AND CASPASE-8. INTERACTS WITH FADD.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
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 CC EMBL; U60315; AAC55287.1; -
 DR EMBL; U68688; AAB57923.1; -
 DR PIR; T30761; T30761.
 DR InterPro; IPR001875; DED.
 DR Pfam; PF01335; DED; 2.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS50168; DED; 2.
 KW Apoptosis; Repeat.
 FT DOMAIN 8 78 DED 1.
 FT DOMAIN 95 175 DED 2.
 SQ SEQUENCE 241 AA; 26939 MW; 155C9F80B969E216 CRC64;

 Query Match 6.8%; Score 122; DB 1; Length 241;
 Best Local Similarity 25.3%; Pred. No. 0.038;
 Matches 37; Conservative 31; Mismatches 48; Indels 30; Gaps 5;
 QY 1 MAEIGEDLDKSDVSL-ITL--MKDYMGKSKSKSPFDLYVELEKLNVAAPDDLDLE 57
 DB 100 MCVGEIDDSERLRAURLFACNLNPLSLSTA-LSESRFVELVALLENGLVSPSSSVLA 158

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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:52:33 ; Search time 118 Seconds

(without alignments)
930.511 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800

Sequence: 1 MAEIGEDLPKSDVSLIFLM.....ITKMDHFFSSUGCILLDVL 348

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 700785

Minimum DB seq length: 0

Maximum DB seq length: 348

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_minc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_podent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	19.2	218	11 Q99MZ5	Q99MZ5 ratius norv
2	277	15.4	78	6 Q8MJ18	Q8MJ18 macaca mula
3	214	11.9	283	13 Q93417	Q93417 gallus gall
4	199	11.1	303	13 Q91B66	Q91B66 xenopus lae
5	193.5	10.8	277	6 Q95ND5	Q95ND5 sus scrofa
6	192.5	10.7	318	13 Q91B65	Q91B65 xenopus lae
7	192	10.7	277	6 Q8MK15	Q8MK15 canis famli
8	190.5	10.6	313	11 Q8CHV5	Q8CHV5 mus musculu
9	190	10.6	328	5 Q8ITP3	Q8ITP3 branchiosto
10	189.5	10.5	277	6 Q8MJU1	Q8MJU1 felis silve
11	187.5	10.4	302	13 Q91B89	Q91B89 oncorhynch
12	186.5	10.4	280	13 Q8JIS9	Q8JIS9 oryzias lat
13	184.5	10.2	182	6 Q77623	Q77623 ovis aries
14	184	10.2	250	13 Q8JIS8	Q8JIS8 oryzias lat
15	182.5	10.1	304	13 Q93415	Q93415 gallus gall
16	177.5	9.9	277	6 Q8MJC3	Q8MJC3 oryctolagus

17	172.5	9.6	276	11 Q9D089	Q9D089 mus musculu
18	172.5	9.6	276	11 Q99M47	Q99M47 mus musculu
19	172.5	9.6	280	11 Q8JG42	Q8JG42 fugu rubrip
20	172	9.6	277	11 Q35397	Q35397 ratius norv
21	172	9.6	243	11 Q9WU16	Q9WU16 ratius norv
22	170.5	9.5	280	13 Q8JGWS	Q8JGWS fugu rubrip
23	169	9.4	312	4 Q8EUV3	Q8EUV3 homo sapien
24	166.5	9.2	289	5 Q8EFL0	Q8EFL0 anopheles s
25	165	9.2	303	11 Q88550	Q88550 ratius norv
26	158.5	8.8	282	13 Q98UI8	Q98UI8 brachydanio
27	152.5	8.5	182	12 Q99CX0	Q99CX0 bovine herp
28	141	7.8	299	5 Q81955	Q81955 spodoptera
29	140	7.8	308	5 Q9NHF9	Q9NHF9 drosophila
30	140	7.8	308	5 Q9VET9	Q9VET9 drosophila
31	134.5	7.5	293	5 Q819V7	Q819V7 bombyx mori
32	130	7.2	189	11 Q8BN14	Q8BN14 mus musculu
33	114.5	6.4	316	5 Q817B0	Q817B0 geodia cydo
34	110	6.1	345	16 Q8E620	Q8E620 streptococc
35	110	6.1	345	16 Q8E0E6	Q8E0E6 streptococc
36	108	6.0	326	5 Q9GV88	Q9GV88 hydra atten
37	108	6.0	345	2 Q54085	Q54085 streptococc
38	107	5.9	188	12 P88961	P88961 kaposi's sa
39	103	5.7	283	13 Q42284	Q42284 gallus gall
40	103	5.7	347	5 Q9GV89	Q9GV89 hydra atten
41	100.5	5.6	344	2 Q57369	Q57369 borrelia bu
42	98	5.4	206	4 Q86WP4	Q86WP4 homo sapien
43	95.5	5.3	335	16 Q7VAV9	Q7VAV9 prochloroco
44	94.5	5.2	104	4 Q9UG96	Q9UG96 homo sapien
45	92	5.1	281	16 Q8XK49	Q8XK49 clostridium

ALIGNMENTS

RESULT 1

Q99MZ5 PRELIMINARY; PRT; 218 AA.
ID Q99MZ5
AC Q99MZ5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE FLIP short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Xiao C.W., Asselin E., Tsang B.K.,
RT "FLIP mRNA expression in rat ovarian granulosa cells.",
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244366; AK28358.1; -
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PSS0168; DED; 2.
SQ SEQUENCE 218 AA; 24718 MW; 9DA9EBAF441967B CRC64;

Query Match 19.2%; Score 345; DB 11; Length 218;
Best Local Similarity 67.3%; Pred. No. 9.2e-20;
Matches 76; Conservative 15; Mismatches 18; Indels 4; Gaps 3;
QY 1 MAEIGEDLPKSDVSLIFLMKDYMGKISKESFLDVLVELEKTLVAPDLDLEKCL 60
DB 102 LMEIGENLQSDVSLIFLTXYTRGKVAKXSLDLVIELEKNTLGSQNLNEKCL 161
QY 61 KNIRHIDLTKIQKQVQAGTSTRNVLAIOK-SLKQPSNNFRE-EPV 110
DB 162 KSIRHIDLTKIQKQVQAGTSTRNVLAIOK-SLKQPSNNFRE-EPV 110

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RESULT 2
ID 08MJ18 PRELIMINARY; PRT; 78 AA.
AC 08MJ18;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Flce/caspase-1 inhibitory protein (Fragment).
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Moneaux V., Ho Tsong Fang R., Hurtrel B., Amelien J.-C.,
RA Estaque J.,
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF530077; AAA95637.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 78 AA; 8971 MW; 6BD208095733A99 CRC64;

Query Match 15.4%; Score 277; DB 6; Length 78;
Best Local Similarity 73.1%; Pred. No. 7.3e-15;
Matches 57; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 86 YRNVLQAAIQKSLKDPSSNFR-----EPPYKSIQSEAFIPQSIPE 127
DB 1 YRNVLQAAIQKSLKDPSSNFRLLHNGRSKQKQLQQLQEPVKTSLQSEAFIPQSIPE 60
QY 128 ERYKKSKKPLGICLITDC 145
DB 61 ERYKKSKKPLGICLITDC 78

RESULT 3
ID 093417 PRELIMINARY; PRT; 283 AA.
AC 093417;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.L., Bridgman J.T.,
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells."
RL Biol. Reprod. 62:589-596 (2000).
DR EMBL, AF083029; AAC32602.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICD_P10.
DR InterPro; IPR001309; ICD_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.

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DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 11.9%; Score 214; DB 13; Length 283;
Best Local Similarity 29.5%; Pred. No. 4.1e-09;
Matches 70; Conservative 31; Mismatches 92; Indels 44; Gaps 8;

QY 101 PSNNPPEPPYKSIQSEAFIPQSIPEERYKKSKPLGICLITDCIGNETELRLDT----- 156
DB 22 PGSKGNLPLSKSVDSG-----ILPDDYENDYIEIGCVYI-----NNKFNHDTGLSS 71
QY 157 -----FTSLGYEQKFLHLSMAGISQILQFACMPERHDYSPFCVLYSRG 202
DB 72 RSGTDAASVREVFMYKLGKYKVLNNDLSRDIPLKLNVS-EEDHSKRSFVCVLLSHG 130
QY 203 GSGSYGVQVQTHSGLELHIRRMFMGDSQPVLAGKPKKFTQNYVYVSGQLDSLSLVD 262
DB 131 DEGLFETD--GPLELKYLTSLFREDKCRSLAGKPLFTD--ACGTGLDSLEADS 184
QY 263 GPAMKWEFAQKRGKCTVHREDFPWSLCTADMSILQSHSPSLYQCLISQKLRQ 319
DB 185 GPD-----ETWCCK-----IPVADPLVAVSTAPGYYSWRNMAEGSWFTQICRMUKE 232

RESULT 4
ID 091B66 PRELIMINARY; PRT; 303 AA.
AC 091B66;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Caspase-6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20209426; Pubmed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.,
RT "Structure, expression and function of the Xenopus laevis caspase
RT family."
RL J. Biol. Chem. 275:10484-10491 (2000).
DR EMBL; AB038169; BAA94747.1; -.
DR HSSP; P42574; ICP3.
DR MEROPS; C14.005; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICD_P10.
DR InterPro; IPR001309; ICD_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34132 MW; 4C54A0A607C69756 CRC64;

Query Match 11.1%; Score 199; DB 13; Length 303;
Best Local Similarity 27.1%; Pred. No. 7.1e-08;
Matches 64; Conservative 41; Mismatches 101; Indels 30; Gaps 9;

QY 99 KDPNNPPEPPYKSIQSEAFIPQSIPEERYKKSKPLGICLITDC----- 144
DB 16 KDSIASENKQKANTVETDGTWTSRTVELDPAFAEYIMTKRGALIFTHEDFYVQLRLG 75
QY 145 -CIGNETEL--LNDTFTSLGYEQKFLHL-SHGISQILQFACMPERHDYSPFCVLYVS 200

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Db 76 SRRGNTDSSNNLNLITLDPDQVQNYNFKTMVLEKI--QENSTDSHNAOCFLCVPLIS 133
QY 201 RGSQSYVGVDOHTSGPLPHIRRMWGDSCPYLAKPKMFEICQNVVSDGQLEDSLL- 259
Db 134 HGEDEKHIVSD---SLIDIGELTNPFKGDCKSLVEXKPIFLIQ---AARGKHDEPVLP 187
QY 260 --EVDGAMKQVVERKAKRGCLCTVHRADPFWSLCTADMSLLEQSHSSPSLYLQCL 313
Db 188 KDEVDSPVLTNTVLT-EVDAASLCTLPAGADPFIMCYSVABGYSHRETVNSWYIIDL 242

RESULT 5

Q95NDS PRELIMINARY; PRT; 277 AA.
AC Q95NDS 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
D 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suidae, Suidae, Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334413; Pubmed=11440638;
RA Muneta Y., Shimojima Y., Mori Y.;
RT "Porcine caspase-3: cloning and its activity during apoptosis of
porcine Pk15 cells induced by porcine Fas-ligand";
RL J. Interferon Cytokine Res. 21:409-415(2001).
DR EMBL; AB029345; BAB55544.1; -
DR MEROPS; C14.003; -
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SMO0115; CASC.1.
DR PROSITE; PS0112; CASPASE_CYS; 1.
DR PROSITE; PS0112; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 10.8%; Score 193.5; DB 6; Length 277;
Best Local Similarity 29.4%; Pred.No.1.8e-07;
Matches 63; Conservative 30; Mismatches 72; Indels 49; Gaps 9;

QY 130 YKMSKPLDGLIIDL-----C-IGNETEL--LRDTFTSLGYEV-----OKF 167
Db 37 YKMDYPMGCIILNNKMPDKTGMACRSQTDVDANLLETFTNLKYEVRNKNQDLTREI 96
QY 168 LHSMEGTSQILQGFACMPERHDYDFVCVLYVSRGSGSYGVDOHTSGPLPHIRRMFM 227
Db 97 LEL-MHSVSK-----EDHSKRSSFICVYLISHGEGKIFG---TNGFVLDLKKLTSFPR 144
QY 228 GDSCEPYLAGPKMFEIC--NYVVSQGLEDSLLSEVDGAMKQVVERKAKRGCLCTVHREA 285
Db 145 GDCRRTLTGPKKFIIDACRGCTELDCGIEFDSDSTEDDMAQCR-----IPVEA 191
QY 286 DFWNSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ 319
Db 192 DFLVAYSTAGYYSWRMSKDGSWFIQSLCALKQ 225

RESULT 6

Q91B65 PRELIMINARY; PRT; 318 AA.
AC Q91B65
DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Caspase-7.
GN XCASPASE-7.
OS Xenopus laevis (African clawed frog).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipidae, Pipidae;
Xenopodidae, Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; Pubmed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038170; BAA94748.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SMO0115; CASC.1.
DR PROSITE; PS0112; CASPASE_CYS; 1.
DR PROSITE; PS0112; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 318 AA; 35937 MW; 6EB06684F86A128 CRC64;

Query Match

Best Local Similarity 10.7%; Score 192.5; DB 13; Length 318;
Pred.No.2.5e-07;
Matches 64; Conservative 39; Mismatches 92; Indels 37; Gaps 10;

QY 111 KKSIOSEAFLEPSI-----PEERYKMSKPLDGLIIDL-----CIG-----NETE 151
Db 48 KKVEDEKPKRTNNNVAIVTAPQYKNNNGVRCIIINNKIKDKITGNGARNGTIDARE 107
QY 152 LMRDTFTSLGYEVQKFLHSMGTSQILQGFACMPERHDYDFVCVLYVSRGSGSYGV 211
Db 108 LIR-CFKGLGFDNVVNNKSCSEMENLITVA--QDDHDSACFACIFLSHGEGGLIYGD 165
QY 212 QTHSGPLPHIRRMWGDSCPYLAKPKMFEIC--NYVVSQGLEDSLLSEVD--GPMK 267
Db 166 ---GAMPIKIVLTILFSGDGRSLVGRKPLFIQACRGHFDG-----LEADSGSYND 215
QY 268 NVEFKQKRGCLCTVHREADPFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ 319
Db 216 SLETDANPRHKIPV--EADFLVAYSTVPGYYSWRNPMGMSWFIQALCSVLNE 265

RESULT 7

Q8WK15 PRELIMINARY; PRT; 277 AA.
AC Q8WK15
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
D 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Caspase-3.
OS Canis familiaris (Dog).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Sano J.;
RT "canine caspase-3 gene";
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB085580; BAB92962.1; -
DR GO; GO:0030693; F:caspase activity; IEA.

DR GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868BDAB9 CRC64;

Query Match 10.7%; Score 192; DB 6; Length 277;
 Best Local Similarity 26.9%; Pred. No. 2.3e-07;
 Matches 64; Conservative 38; Mismatches 92; Indels 44; Gaps 8;

QY 102 SNRFEPEPVK---KSIQSEAFLPQSIPEBRYKSKPLGICLIID----- 144
 DB 10 AKSFNAETKILHGSKSDGMSF-----DNGYKMDYPEMGICIIINKNPFKSTGMAP 63
 QY 145 CIGNTEL--LRDFTSLGYEVQKFLHSMHGISQILGQFACMPEHRDYSFVCVLSRG 202
 DB 64 RSGTVDVDAANLRFTTNKLVKRNKNDLTCEELIELNVS-KEDHSKSSFCVLSHG 122
 QY 203 GSQVYGVDTHTSGLPPLHHRMFMGDSCPYLAKPKMFIQ--NYVSDQLEDSLLIE 260
 DB 123 DEGIIFG---INGPYDAARKVGFPRGDCRSILTKPPLFIQCRGTELDGCIEIDSGIE 179
 QY 261 VDGPAMKVERKAGKRGCTHREADPFWSLCTADMSLLEQSHSSPSLYLOCSQKLR 318
 DB 180 DDMACQK-----IPVADFLVAYSTAPGYYSWRNSKDSWFIQSLCMLK 224

RESULT 8

ORCHVS PRELIMINARY; PRT; 313 AA.

AC 08CHVS; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Caspase 3, apoptosis related cysteine protease (Fragment).
 GN CASP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Strausberg R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC038825; AAH38825.1; -
 DR MGD; MGI:107739; Casp3.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006503; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Protease.
 FT NON TER
 SQ SEQUENCE 313 AA; 35174 MW; 96B98A1F04E769FC CRC64;

Query Match 10.6%; Score 190.5; DB 11; Length 313;
 Best Local Similarity 28.5%; Pred. No. 3.6e-07;

Matches 75; Conservative 40; Mismatches 107; Indels 41; Gaps 13;
 QY 76 KQSVQAGT---SYRWLQAAIQSLKDPSSNNFREEPV--KSIQSEAFLPQSIPEER 129
 DB 19 KRSVLRGAMNGTLRVTYENNNKTSVSDSINNFEVKTHSGSKV-DGIIYLDSS----- 72
 QY 130 YKXKSKRPLGICLIID-----CIGNTEL--LRDFTSLGYEVQKFLHSMHG 175
 DB 73 YKMDYPEMGICIIINKNPFKSTGMSRSGTVDVDAANLRFTFMGLKYQVRKNDLTREDI 132
 QY 176 SQLGQFACMPEHRDYSFVCVLSRGSGSQSYGVDTHTSGLPPLHHRMFMGDSCPYLA 235
 DB 133 LEIUDSVS-KEDHSKSSFCVLSHGDEGVYQ---INGPYELKLTNSFRGDYCRSLT 188
 QY 236 GKPRMFIQNYVSDQLEDSLLIEVDGPAMKVERKAGKRGCTHREADPFWSLCTAD 295
 DB 189 GKPLFLIQ---ACRGTELDG-IETDSGT--DEMACQK-----IPVADFLVAYSTAP 237
 QY 296 MSLLQSHSPSLYLQCSQKLR 318
 DB 238 GYYSWRNSKDSWFIQSLCMLK 260

RESULT 9

Q8ITP3 PRELIMINARY; PRT; 328 AA.

AC Q8ITP3; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Amphicasp-3/7.
 DE Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TaxID=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22217375; PubMed=12232796;
 RA Bayascas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,
 RA Comella J.X.;
 RT "Isolation of Amphicasp-3/7, an ancestral caspase from amphioxus
 (Branchiostoma floridae). Evolutionary considerations for vertebrate
 caspases.";
 RT caspases.";
 RL Cell Death Differ. 9:1078-1089(2002).
 DR EMBL; AF412335; AAN45849.1; -
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001309; ICE_p10.
 DR InterPro; IPR002138; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 328 AA; 36327 MW; 1D46760AFA71845B CRC64;

Query Match 10.6%; Score 190; DB 5; Length 328;
 Best Local Similarity 32.7%; Pred. No. 4.1e-07;
 Matches 55; Conservative 24; Mismatches 77; Indels 12; Gaps 6;

QY 157 FTSLGVEVQKFLHSMHGISQILGQFACMPEHRDYSFVCVLSRGSGSYGVDTHTSG 216
 DB 120 FSKLGFEFTKVPDNLCKILSVL-QLAARDHRDVCFCALISHGEBGVIGTD---GH 175
 QY 217 LPLHHRMFMGDSCPYLAKPKMFIQNYVSDQLEDSLLIEVDGP--AMKNEFKAK 275
 DB 176 MEVTEVTKPRGRCPELVGKPLFLQ---ACRGNEFHG---VMDPALREVQDDELDA 229
 QY 276 RGLCTVREADPFWSLCTADMSLLEQSHSSPSLYLOCSQKROERKGT 323

Db 230 GNRKTLAEADFLIANTVPGYYSWRNPGRGSWYIQAALCAVIERE-GT 276

RESULT 10

OSMUT1 PRELIMINARY; PRT; 277 AA.

AC OSMUT1

DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Caspase3.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

NCBI_TaxId=9685;

Sequence from N.A.

RA Yamazaki J., Sano R., Hasegawa A.;

RL "Felis catus mRNA for caspase3, complete cds.";

RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB090246; F:caspace activity; IEA.

DR GO: GO:0030693; F:caspace activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE_p20.

DR InterPro: IPR002398; Peptidase C14.

DR Pfam: PF00656; Peptidase C14; I.

DR PRINTS: PR00376; ILIBENZYME.

DR SMART: SM00115; CASc; 1.

DR PROSITE: PS01121; CASPASE_CYS; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

SC SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;

Query Match 10.4%; Score 189.5; DB 6; Length 277;

Best Local Similarity 27.8%; Pred. No. 3,7e-07;

Matches 66; Conservative 35; Mismatches 83; Indels 53; Gaps 9;

Qy 112 KSIOESAPF---PQSIPI-----EERYKMKSKRIGICLIID-----CIGNETE 151

Db 11 KSISKSETKIFHSGSKMDSGITYNDNSYKMDYPMGICLIINKNFHESTGMPRSSTVD 70

Qy 152 L--LRDFTSLGYEVOKFHLTSMHGISOILGQFACPEHRDPSFVCYLVRGSGSQSYG 209

Db 71 AANLRFTFLTKYEVRANKNDLTREQIVALLDSVS-REDHSKRSFICVLSHGEEGIY 129

Qy 210 VDTQHSGLPLHTRKRMGNSCPYLAKRKMFIQNY-----VSDGLEDSLLLEV 261

Db 130 ---TNGVVDIKKLTGFFRGYCRSLGKPKLFIQAQCRGTLDGCIETDSTED----- 180

Qy 262 DGPAMKVEFKAKRGICTVHREADFFWGLCTADMSLLEQSHSSPSLYLQCLSQKLR 318

Db 181 -----DIACK-----IPVADFLVAVSTHPGYYSWRNKGDSWFIQSLCSMLR 224

RESULT 11

Q918S9 PRELIMINARY; PRT; 302 AA.

AC Q918S9

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Caspase 6.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Butelosteii;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NCBI_TaxId=8022;

Sequence from N.A.

RA Laine K.J., Holland J., Bonilla S., Cunningham C., Secombes C.D.;

RT "Cloning and sequencing of caspase 6 in rainbow trout, *Oncorhynchus*

RT mykiss, and analysis of its expression under conditions known to induce apoptosis.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF212219; AAF73848.1; -

DR HSSD: P42574; 1PAU.

DR MER068; C14.005; -.

DR GO: GO:0030693; F:caspace activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE_p20.

DR InterPro: IPR002398; Peptidase C14.

DR Pfam: PF00656; Peptidase C14; I.

DR PRINTS: PR00376; ILIBENZYME.

DR SMART: SM00115; CASc; 1.

DR PROSITE: PS01121; CASPASE_CYS; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

SC SEQUENCE 302 AA; 34082 MW; 5AB5F28ACFA660 CRC64;

Query Match 10.4%; Score 187.5; DB 13; Length 302;

Best Local Similarity 25.0%; Pred. No. 5,9e-07;

Matches 69; Conservative 38; Mismatches 110; Indels 59; Gaps 10;

Qy 67 DLKTKIQYKQAGVAGTSYRVVLQAIOKSLKDPNNFREPVKKSIOESAPFQSI- 125

Db 8 DTGSLKQNKTSQTTG-----PSEN-----ITETDGFCSSSF 41

Qy 126 ---PEERYKMKSKRIGICLIID-----CIGNETELRDTFTSLGYEVOKF 167

Db 42 SMDPAEYVQNRKRLALIFQEHFVHLMPRPNGNADRSNLVK-RFDLNEVQAF 100

Qy 168 LHLTSMHGISOILGQF--ACPEHRDYDSFVCYLVRGSGSQSYGVDTQHSGLPLHTRM 225

Db 101 DNLR--VEEVLDSQAANAHADACFVCFVLSHGENDHYAYDNR--IAIDITAL 154

Qy 226 FNGDSCPYLAGKPKMFIQNYVVSDDLESSL--LEVDPAMKVEFKAKRGICTVH 283

Db 155 FKGDKSKSLVGKPKFIQ--ACRGDKHDPVTMDVDSVKTNEVAVAGVYITLPA 211

Qy 284 EADFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQ 319

Db 212 GADFIWCYSAAGYVSHRETLINGSWYIQLDLCAMRK 247

RESULT 12

Q9JIS9 PRELIMINARY; PRT; 280 AA.

AC Q9JIS9

DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Caspase 3B.

OS Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Belontiiformes; Atherinichthyidae; Oryziinae; Oryzias.

NCBI_TaxId=8090;

Sequence from N.A.

RA MEDLINE=20211495; PubMed=10747068;

RA Naruse K., Fukumachi S., Mitani H., Kondo M., Matsuo K., Kondo S., Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A., Wada H., Kusabe T., Suzuki N., Kinoshita M., Kanamori A., Terado T., Kimura H., Nonaka M., Shima A.;

RT "A Detailed Linkage Map of Medaka, *Oryzias latipes*: Comparative Genomics and Genome Evolution."

RL Genomics 154:1773-1784(2000).

DR EMBL: AB032608; BAC00948.1; -

DR GO: GO:0030693; F:caspace activity; IEA.

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE p20.
 DR InterPro: IPR002398; Peptidase C14.
 DR Pfam: PF00656; Peptidase C14; 1.
 DR PRINTS: PR00376; TLIBCNZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 280 AA; 31168 MW; 5095512F1E485542 CRC64;

Query Match 10.4%; Score 186.5; DB 13; Length 280;
 Best Local Similarity 27.5%; Pred. No. 6.5e-07;
 Matches 61; Conservative 26; Mismatches 74; Indels 61; Gaps 9;

QY 129 RYKMSKRLGICLIIDICNETELLRD-----FTSLGYEVQKFLHL 170
 DB 43 RYSLNFTPTGLCIIT---NNKNPDRGTGMNNGNDIDASAMKVFSLGIVRYKTYNQ 98
 QY 171 SMGISQILGQFACMPHRDYDSFVCLVSRGSGSYGVDTGSHGLPLHIRRMFGDS 230
 DB 99 TVKQIKQLITVSRM-DHSDASFCILSHGEGVFFGTD--GSIEIKLTLSLFRGDH 154
 QY 221 CEYLAGKPMFFIQQ-NYVSDGQLSDSLLEVDPGPMKNVEFKAQKRGICTVHREADFWS 290
 DB 155 CKSLGKPKLFFIQ-ACRGTEIDDG--IEAD-----SKEDTKIPVEADFLYA 199
 QY 231 LCTADMSLLEQSHSPSLYLQCLSQKLRGRTIPSGSITES 332
 DB 200 FSTA-----PGY-----SWRNTWTGSMFIN 221

RESULT 13

077623 PRELIMINARY; PRT; 182 AA.

AC 077623;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Caspase-3 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rueda B.R., Hendry I.R., Tilly J.L., Hamernik D.L.,
 RT "Accumulation of Caspase-3 mRNA and induction of Caspase Activity in
 the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment in
 Vivo";
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF068837; AAC25713.1; --
 DR HSSP; P42574; IPAU.
 DR MEROPS; C14.003; --
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE p10.
 DR InterPro: IPR001309; ICE p20.
 DR InterPro: IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 FT NON TER 1 1
 SQ SEQUENCE 182 AA; 20408 MW; B5860C6996C21BE7 CRC64;

Query Match 10.2%; Score 184.5; DB 6; Length 182;
 Best Local Similarity 31.0%; Pred. No. 5.5e-07;
 Matches 57; Conservative 27; Mismatches 67; Indels 33; Gaps 7;

QY 127 EERYKKSKRLGICLIID-----C-IGNETEL--LRDTFTSLGYEVQKFLHSM 172
 DB 3 EESYQDPEYMEGICLIINNKNFNHNTGMACRGDTVDADANIREFTFTSLKYVRIRKNDLTR 62
 QY 173 HGSISQILGQFACMPHRDYDSFVCLVSRGSGSYGVDTGSHGLPLHIRRMFGDSCP 232
 DB 63 KEMLEMSDVS-KEDSKRSSTFCILSHGEGVFFGTD--INGPDLXKLASFRRGDCC 118
 QY 233 YLAGKPMFFIQQ-NYVSDGQLSDSLLEVDPGPMKNVEFKAQKRGICTVHREADFWS 290
 DB 119 SLTGKPKLFFIQACRGTEIDCGIFETDSGEDDMACQK-----IPVEADFLYA 165
 QY 291 LCTA 294
 DB 166 YSTA 169

RESULT 14

080158 PRELIMINARY; PRT; 290 AA.

AC 080158;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Caspase 3A.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20211495; PubMed=10747068;
 RA Natuse K., Fukamachi S., Mitani H., Kondo M., Matsuo T., Kondo S.,
 RA Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
 RA Wada H., Kusakabe T., Suzuki N., Kinoshita M., Kanamori A., Terado T.,
 RA Kimura H., Nonaka M., Shima A.;
 RT "A detailed linkage map of Medaka, Oryzias latipes: Comparative
 Genomics and Genome Evolution";
 RL Genetics 154:1773-1784 (2000).
 DR EMBL; AB032609; BAC0949.1; --
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE p10.
 DR InterPro: IPR001309; ICE p20.
 DR InterPro: IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; TLIBCNZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 290 AA; 32686 MW; D8C3BC00D32E846C CRC64;

Query Match 10.2%; Score 184; DB 13; Length 290;
 Best Local Similarity 25.4%; Pred. No. 1.1e-06;
 Matches 62; Conservative 41; Mismatches 99; Indels 42; Gaps 7;

QY 97 SLNDPSN-NFREPPYKKSIOSEAFPLPSIEERYKMSKRLGICLI----- 143
 DB 23 SKSPANQPPRPRTDYCVKKQDAPF-----RSMQYPPKGCICLIINNKNPFKDSGM 74
 QY 144 ---DCIGNETELLRDFTFTSLGYEVQKFLHLSMGSISQILGQFACMPHRDYDSFVCLVS 200
 DB 75 GFRNGTDNDAAAMKSFMKLGYEIQYXNQYDQMKLFRQMS-NQDSKRFASFACVILS 133
 QY 201 RGSQSYGVDTGSHGLPLHIRRMFGSCPYLAGKPMFFIQQNYVSDGQLSDSLLE 260
 DB 134 HGEQGVYGTD---GPVSFKLIECLKSGSLSLVKPKLFFIQ--ACRGLFD----- 182
 QY 261 VDPGPMKNVEFKAQKRGICTVHREADFWSLCTADMSLLEQSHSPSLYLQCLSQKLR 320

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 8, 2004, 05:51:33; Search time 128 Seconds
(without alignments)
768.176 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDDKSVSLIFLM.....ITSEKDMHFSSLGICLLDVL 348

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1312285

Minimum DB seq length: 0
Maximum DB seq length: 348

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq_29Jan04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1800	100.0	348	2	AAW69230 I-FLICE-2
2	1800	100.0	348	7	ADA10619 Human inh
3	1229	68.3	302	2	AAV05792 WRIT-ND1
4	1128	62.7	264	2	AAV05792 Human ant
5	978	54.3	230	2	AAV05793 MRIT-Bam
6	711.5	39.5	291	3	AAV67420 Usurpin-9
7	683	37.9	175	2	AAV05794 MRIT-D/S
8	661.3	36.8	270	5	AAE26110 Human FLA
9	540	30.0	227	2	AAV05795 WRIT Delta
10	527	29.3	221	2	AAW78904 Human GI
11	527	29.3	221	2	AAW78904 Human GI
12	527	29.3	221	2	AAV05789 Human MAC
13	527	29.3	221	2	AAV57455 Human FLI
14	527	29.3	221	3	AAV03959 FLICE-11k
15	527	29.3	221	4	AAV03959 FLICE-11k
16	527	29.3	221	4	AAV03959 FLICE-11k
17	527	29.3	221	5	AAV03959 FLICE-11k
18	391	21.7	76	4	AAV5359 Peptide #
19	391	21.7	76	4	AAV5359 Peptide #
20	391	21.7	76	4	AAV5359 Peptide #
21	391	21.7	76	4	AAV5359 Peptide #
22	391	21.7	76	4	AAV5359 Peptide #
23	391	21.7	76	4	AAV5359 Peptide #
24	391	21.7	76	4	AAV5359 Peptide #
25	391	21.7	76	4	AAV5359 Peptide #

25	391	21.7	76	4	AAV03118	AAV03118 Peptide #
27	391	21.7	76	5	AAV37140	AAV37140 Human pep
28	383	21.3	84	4	AAV4787	AAV4787 MRIT deat
29	369	20.5	84	4	AAV61102	AAV61102 Human MRI
30	337	18.7	218	5	AAV09296	AAV09296 Mouse FLI
31	228	12.7	286	3	AAV56997	AAV56997 Human pro
32	228	12.7	286	3	AAV59578	AAV59578 Human cas
33	225	12.5	254	4	AAV98656	AAV98656 Caspase-8
34	215	11.9	266	2	AAV11896	AAV11896 MACH Isot
35	199	11.1	293	2	AAV05244	AAV05244 Apoptotic
36	199	11.1	293	2	AAV21720	AAV21720 Amino aci
37	199	11.1	293	2	AAV06063	AAV06063 Human cas
38	199	11.1	293	5	AAV021925	AAV021925 Human cas
39	199	11.1	293	5	AAV01221	AAV01221 Human cas
40	193.5	10.8	277	4	AAV78712	AAV78712 Pig caspa
41	190	10.6	231	5	AAV42451	AAV42451 Human ova
42	189.5	10.5	167	4	AAV31155	AAV31155 Peptide #
43	189	10.5	261	4	AAV0610	AAV0610 Chimeric
44	188.5	10.5	277	4	AAV05395	AAV05395 Mouse cas
45	187.5	10.4	278	3	AAV85061	AAV85061 Interleuk

ALIGNMENTS

RESULT 1
ID AAW69230 standard; protein; 348 AA.
AAW69230:
18-FEB-1999 (first entry)
I-FLICE-2 protein.
I-FLICE-2 protein.
I-FLICE-2: PADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
viral infection; head injury; cancer; autoimmune disorder; therapy;
viral infection; graft versus host disease; graft rejection.
Homo sapiens.
WO9831801-A1.
23-JUL-1998.
21-JAN-1998; 98WO-US000969.
21-JAN-1997; 97US-0034205P.
05-AUG-1997; 97US-0054800P.
(HUMA-) HUMAN GENOME SCI INC.
(UNMI) UNIV MICHIGAN.
N1 J, Rosen CA, Dixit VM, Gentz RL, Kenny JI;
WPI, 1996-414100/35.
N-PSDB; AAV4807.
New inhibitory polypeptides of FLICE - used to develop products for
treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
autoimmune disorders, viral infection or graft rejection.
Claim 9, Fig 4, 118pp; English.
This sequence is an inhibitor of Fas-ligand associated with death
domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-2. The
proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
the first examples of a naturally occurring catalytically inactive
caspase that can act as a dominant negative inhibitor of apoptosis. The
polypeptides and agonists can be used for treating e.g. Alzheimer's
disease, Parkinson's disease, rheumatoid arthritis, sepsis,

CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
CC cell death associated with cardiovascular disease, polycystic kidney
CC disease, apoptosis of endothelial cells in cardiovascular disease,
CC degenerative liver disease, multiple sclerosis (MS) and head injury
CC damage. Antagonists of the polypeptides can be used for treating cancers
CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
CC adenoviruses), graft versus host disease, acute disease, acute graft
CC rejection, and chronic graft rejection. The products can also be used for
CC detection, diagnosis and drug screening

CC Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 5.6e-172; Indels 0; Gaps 0;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKEKSFLLDVELEKLNVAAPQDLLEKCL 60
Db 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKEKSFLLDVELEKLNVAAPQDLLEKCL 60
QY 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQKSLKDPNNFREBPVKKSIOESEAF 120
Db 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQKSLKDPNNFREBPVKKSIOESEAF 120
QY 121 LPSGIPERRYKMKSPKPLGICLIIDICIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
Db 121 LPSGIPERRYKMKSPKPLGICLIIDICIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
QY 181 QPACMEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLPHIRRMFMGDSCPYLAGPKM 240
Db 181 QPACMEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLPHIRRMFMGDSCPYLAGPKM 240
QY 241 FFIQNVVSDGQLSDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
Db 241 FFIQNVVSDGQLSDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
QY 301 QSHSSPSLYLQCLSQKLRQERGITPGSGITESKDMHFSSIGCILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERGITPGSGITESKDMHFSSIGCILLDVL 348

RESULT 2

ADA10619 standard; protein; 348 AA.

ADA10619;

06-NOV-2003 (first entry)

Human inhibitor of FLICE (I-FLICE-2) protein.

Human; I-FLICE-2; inhibitor of FLICE; FADD-like ICE;
tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
CD-95 induced apoptosis; apoptosis associated disease;
Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
ischaemia; septic shock; degenerative liver disease;
cardiovascular disorder; aberrant cell survival; noctropic;
antirheumatic; vasotropic; hepatotropic; osteopathic; cardiac;
cerebroprotective; antibacterial; antiarthritic; vasodilator.

Homo sapiens.

US2003087339-A1.

08-MAY-2003.

21-JAN-1998; 98US-00009893.

21-JAN-1997; 97US-0034205P.

PR 05-AUG-1997; 97US-0054800P.

PA (NTUJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (DIXI/) DIXIT V M.
PA (GENTZ/) GENTZ R L.
PA (KENNY/) KENNY J J.

PI NI J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;

DR WPI; 2003-576674/54.

DR N-PSDB; ADA10618.

PT New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
PT for treating diseases associated with apoptosis e.g., Alzheimer's
PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
PT shock.

XX Claim 1; Fig 4A-4C; 48pp; English.

The present invention relates to the isolation of novel human I-FLICE-1
CC (inhibitor of FLICE (FADD-like ICE) and I-FLICE-2 proteins, and the
CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
CC and recombinant methods for producing the I-FLICE proteins. The sequences
CC and methods are useful for treating diseases associated with apoptosis
CC e.g. Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
CC disorders. They are also useful for diagnosing diseases or disorders
CC associated with aberrant cell survival in an individual. The present
CC sequence represents human I-FLICE-2.

XX Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 7; Length 348;
Best Local Similarity 100.0%; Pred. No. 5.6e-172; Indels 0; Gaps 0;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKEKSFLLDVELEKLNVAAPQDLLEKCL 60
Db 1 MAEIGEDLDKSDVSLIFLMKDVMGRKISKEKSFLLDVELEKLNVAAPQDLLEKCL 60
QY 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQKSLKDPNNFREBPVKKSIOESEAF 120
Db 61 KNHRIIDLTKIQKQKOSVQAGTSYRNVLQAAIQKSLKDPNNFREBPVKKSIOESEAF 120
QY 121 LPSGIPERRYKMKSPKPLGICLIIDICIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
Db 121 LPSGIPERRYKMKSPKPLGICLIIDICIGNETELRDFTSLGYEVQKFLHSMHGISOILG 180
QY 181 QPACMEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLPHIRRMFMGDSCPYLAGPKM 240
Db 181 QPACMEHRDYSFVCVLVSRGSGSVYGVQDTHSGPLPHIRRMFMGDSCPYLAGPKM 240
QY 241 FFIQNVVSDGQLSDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
Db 241 FFIQNVVSDGQLSDSSLSLEVDPAMKNVEFKAQKGLCTVHREAPFMSLCTADMSLLE 300
QY 301 QSHSSPSLYLQCLSQKLRQERGITPGSGITESKDMHFSSIGCILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERGITPGSGITESKDMHFSSIGCILLDVL 348

RESULT 3

AAV05792 standard; protein; 302 AA.

AAV05792;

02-AUG-1999 (first entry)

MRIT-ND1 polypeptide.

XX MRIT-ND1, MACH related inducer of toxicity; human; apoptosis;
 KM anti-apoptotic; cancer; autoimmune disease; angiogenesis;
 KM atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KM Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
 KM aplastic anaemia; myocardial infarction; therapy; mutant.

XX Homo sapiens.
 OS Synthetic.

XX W09918230-A2.

XX 15-APR-1999.

XX 07-OCT-1998; 98MO-US021132.

XX 07-OCT-1997; 97US-00946226.

XX (UNIW) UNIV WASHINGTON.

XX Chaudhary PM;

XX WPI; 1999-277275/23.

XX Identifying regulators of MACH-related inducer of toxicity.

XX Example 2; Page; 78pp; English.

XX The present sequence represents MRIT-ND1, comprising amino acid residues
 CC 179-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see
 CC AA05787). This deletion mutant was used to examine the interaction of
 CC MRIT alpha 1 with caspases. The results indicated that FLIC-p20 binding
 CC to MRIT alpha 1 does not require the N-terminal 179 amino acids. The
 CC invention provides multiple isoforms of MRIT (see AA05787-89), isolated
 CC active fragments of which have either pro-apoptotic or anti-apoptotic
 CC activity. Selective enhancers and inhibitors of MRIT apoptotic activity
 CC can be identified and used to treat diseases mediated by the dysfunction
 CC of programmed cell death or proliferation, such as cancer or a
 CC neurodegenerative disorder. Note: the present sequence is not shown in
 CC the specification but is derived from the MRIT alpha 1 sequence given in
 CC figure 1F

XX Sequence 302 AA;

Query Match 68.3%; Score 1229; DB 2; Length 302;
 Best Local Similarity 92.2%; Pred. No. 1.2e-114;
 Matches 237; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 83 GTSYRVNLQAALQKSLKDPNNR-----EEVYKSIQSEAFLPQS 124

DB 1 GTSYRVNLQAALQKSLKDPNNRFLHNGSKSKORLKEQIGAQQEPYKKSIOSEAFLPQS 60

QY 125 IPEERYKMSKPLGLIILIDICIGNETELDRDFTSLGYEVQKFLHLSMHGISQILGQFAC 184

DB 61 IPEERYKMSKPLGLIILIDICIGNETELDRDFTSLGYEVQKFLHLSMHGISQILGQFAC 120

QY 185 MPKHRYDSEVYCVLVSRGSSQSYGVDTQHSGLPLHHRMFMGSCYLLAGKPMFEITQ 244

DB 121 MPKHRYDSEVYCVLVSRGSSQSYGVDTQHSGLPLHHRMFMGSCYLLAGKPMFEITQ 180

QY 245 NYVVSQGLDESSLLEVDGPANKNVEFKAQKRGKGLCTVHREADFWSLCTADMSLLEQSHS 304

DB 181 NYVVSQGLDESSLLEVDGPANKNVEFKAQKRGKGLCTVHREADFWSLCTADMSLLEQSHS 240

QY 305 SPSLYLCQLSOKLRQER 321

DB 241 SPSLYLCQLSOKLRQER 257

RESULT 4

AA05790 standard; protein; 264 AA.

XX AA05790 standard; protein; 264 AA.

AC AA05790;
 XX 02-AUG-1999 (first entry)
 DT
 XX Human anti-apoptotic MRIT-ND2 fragment.

XX MRIT-ND2, MACH related inducer of toxicity; human; apoptosis;
 KM anti-apoptotic; cancer; autoimmune disease; angiogenesis;
 KM atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KM Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
 KM aplastic anaemia; myocardial infarction; therapy; mutant.

XX Homo sapiens.

OS Synthetic.

XX W09918230-A2.

XX 15-APR-1999.

XX 07-OCT-1998; 98MO-US021132.

XX 07-OCT-1997; 97US-00946226.

XX (UNIW) UNIV WASHINGTON.

XX Chaudhary PM;

XX WPI; 1999-277275/23.

XX Identifying regulators of MACH-related inducer of toxicity.

XX Claim 17; Page; 78pp; English.

XX The present sequence represents MRIT-ND2, comprising amino acid residues
 CC 217-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see
 CC AA05787). MRIT-ND2 has anti-apoptotic activity, as exemplified by the
 CC ability to suppress apoptosis mediated by a TNF family receptor in BHK or
 CC HeLa cells. The invention provides multiple isoforms of MRIT (see
 CC AA05787-89), isolated active fragments of which have either pro-
 CC apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
 CC of MRIT apoptotic activity can be identified and used to treat diseases
 CC mediated by the dysfunction of programmed cell death or proliferation. A
 CC cell accumulation disorder such as cancer, autoimmune disease, viral
 CC infection, angiogenesis or atherosclerosis is treated by administering an
 CC agent that selectively enhances MRIT apoptotic activity, thereby inducing
 CC apoptosis in a subject. A disorder of cell loss, such as a
 CC neurodegenerative disorder, including Alzheimer's disease, Parkinson's
 CC disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
 CC infarction or AIDS is treated by administering an agent that selectively
 CC inhibits MRIT apoptotic activity. Note: the present sequence is not shown
 CC in the specification but is derived from the MRIT alpha 1 sequence given
 CC in figure 1F

XX Sequence 264 AA;

Query Match 62.7%; Score 1128; DB 2; Length 264;
 Best Local Similarity 98.6%; Pred. No. 1.5e-104;
 Matches 213; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 106 REEPYKKSIOSEAFLPQSIPEERYKMSKPLGLIILIDICIGNETELDRDFTSLGYEVQ 165

DB 4 QOEPYKKSIOSEAFLPQSIPEERYKMSKPLGLIILIDICIGNETELDRDFTSLGYEVQ 63

QY 166 KFLHLSMHGISQILGQFACMPKHRYDSEVYCVLVSRGSSQSYGVDTQHSGLPLHHRM 225

DB 64 KFLHLSMHGISQILGQFACMPKHRYDSEVYCVLVSRGSSQSYGVDTQHSGLPLHHRM 123

QY 226 FPGDSCPYLAGKPMFTQNYVVSQGLDESSLLEVDGPANKNVEFKAQKRGKGLCTVHREA 285

DB 124 FPGDSCPYLAGKPMFTQNYVVSQGLDESSLLEVDGPANKNVEFKAQKRGKGLCTVHREA 183

QY 286 DFFWSLCTADMSLLEQSHSPSLYLCQLSOKLRQER 321

Db 184 DFWSLCTADMSLLEQSHSPSYLQCLQSLRQER 219

RESULT 5
AAV05793
ID AAV05793 standard; protein, 230 AA.
XX
AC AAV05793;
XX
DT 02-AUG-1999 (first entry)
XX
DE MRIT-Bam polypeptide.
XX
KW MRIT-Bam; MACH related inducer of toxicity; human; apoptosis;
KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
KW aplastic anaemia; myocardial infarction; therapy; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9918230-A2.
XX
PD 15-APR-1999.
XX
PF 07-OCT-1998; 98WO-US021132.
XX
PR 07-OCT-1997; 97US-00946226.
XX
PA (UNIT) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-277275/23.
XX
PT Identifying regulators of MACH-related inducer of toxicity.
XX
PS Example 2; Page; 78pp; English.
XX
XX The present sequence represents MRIT-Bam, comprising amino acid residues
CC 251-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see
CC AAV05787). This deletion mutant was used to examine the interaction of
CC MRIT alpha 1 with caspases. The results indicated that FLICE-920 binding
CC to MRIT alpha 1 does not require the N-terminal 215 amino acids. The
CC invention provides multiple isoforms of MRIT (see AAV05787-89), isolated
CC active fragments of which have either pro-apoptotic or anti-apoptotic
CC activity. Selective enhancers and inhibitors of MRIT apoptotic activity
CC can be identified and used to treat diseases mediated by the dysfunction
CC of programmed cell death or proliferation, such as cancer or a
CC neurodegenerative disorder. Note: the present sequence is not shown in
CC the specification but is derived from the MRIT alpha 1 sequence given in
CC figure 1f
XX
SQ Sequence 230 AA;
XX
Query Match 54.3%; Score 978; DB 2; Length 230;
Best Local Similarity 99.5%; Pred. No. 1.5e-89;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 137 LGICLIIDICIGNETELLDPTSLGVEYQKFLHSMGISOILGQFACMPERHDYDFVC 196
1 LGICLIIDICIGNETELLDPTSLGVEYQKFLHSMGISOILGQFACMPERHDYDFVC 60
XX
Db 197 VLVSRCGSGSYGVVDQTHSGPLPIHIRMFGDSCPLAKPKMFIQNYVVDGQLDLS 256
61 VLVSRCGSGSYGVVDQTHSGPLPIHIRMFGDSCPLAKPKMFIQNYVVDGQLDLS 120
XX
Db 257 SLLEVDGPAKKNVEFKAKRGKLCYHREADFFNSLCTADMSLLEQSHSPSYLQCLQSL 316
121 SLLEVDGPAKKNVEFKAKRGKLCYHREADFFNSLCTADMSLLEQSHSPSYLQCLQSL 180
XX
QY 317 LRQER 321

Db 181 LRQER 185

RESULT 6
AAV67420
ID AAV67420 standard; protein, 291 AA.
XX
AC AAV67420;
XX
DT 12-MAY-2000 (first entry)
XX
DE Usurpin-gamma polypeptide.
XX
KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
KW caspase; cytosolic; antiParkinsonian; antidiabetic.
XX
OS Homo sapiens.
XX
PN WO200003023-A1.
XX
PD 20-JAN-2000.
XX
PF 07-JUL-1999; 99WO-CA000615.
XX
PR 08-JUL-1998; 98US-0092005P.
XX
PA (MERI) MERCK FROST CANADA INC.
XX
PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
XX
DR WPI; 2000-160929/14.
XX
PR N-PSDB; AAZ56989.
XX
PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
PT disease.
XX
PS Claim 6; Fig 11B; 69pp; English.
XX
XX The invention provides recombinant nucleic acid molecules encoding
CC usurpin-alpha (lacking the first death effector domain (DED) or its
CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
CC useful for in vitro and in vivo identification of usurpin-procaspase-8
CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
CC of cells to CD95 (Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
CC is useful for treating diseases like autoimmune diabetes, cancer and
CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
CC interaction are also useful for treating various diseases mediated by
CC apoptosis. Usurpin provides an attractive model for modulating caspase
CC activation. Sensitivity of cells bearing CD95 (Fas/Apo-1) receptor can be
CC regulated at several levels in the presence of usurpin, conferring
CC resistance to Fas-ligand cell death. The present sequence represents the
CC usurpin-gamma polypeptide
XX
SQ Sequence 291 AA;
XX
Query Match 39.5%; Score 711.5; DB 3; Length 291;
Best Local Similarity 87.5%; Pred. No. 1.3e-62;
Matches 147; Conservative 1; Mismatches 1; Indels 19; Gaps 2;

Db 1 MAEIGEDLDSDVSSILFLMKQYMGKSKSKSFIDLVELEKINLVAPODLLEKCL 60
97 MAEIGEDLDSDVSSILFLMKQYMGKSKSKSFIDLVELEKINLVAPODLLEKCL 155
XX
Db 61 KNIHRIIDLKTKIKYKQSYQAGTSYRNTLQAAIQKSLKDPSSNFR----- 106
156 KNIHRIIDLKTKIKYKQSYQAGTSYRNTLQAAIQKSLKDPSSNFR----- 215
XX
QY 107 ----EPVYKSIQSEAFIPQSTPEERYKPKSKPLGICLIIDICIGNET 150
216 LGAQQEPVYKSIQSEAFIPQSTPEERYKPKSKPLGICLIIDICIGNET 263

RESULT 7

AA05794
ID AA05794 standard; protein: 175 AA.

AC AA05794;

02-AUG-1999 (first entry)

MRIT-D/S polypeptide.

MRIT-D/S; MACH related inducer of toxicity; human; apoptosis;
anti-apoptotic; cancer; autoimmune disease; angiogenesis;
atherosclerosis; neurodegenerative disease; Alzheimer's disease;
Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
aplastic anaemia; myocardial infarction; therapy; mutant.

OS Homo sapiens.
XX Synthetic.

XX WO9918230-A2.
XX 15-APR-1999.

XX 07-OCT-1998; 98MO-US021132.
XX 07-OCT-1997; 97US-00946226.

XX 07-OCT-1997; 97US-00946226.
XX (UNIM) UNIV WASHINGTON.

XX Chaudhary PM;
XX WPI; 1999-277275/23.

XX Identifying regulators of MACH-related inducer of toxicity.
XX Example 2; Page: 78pp; English.

The present sequence represents MRIT-D/S, comprising amino acid residues 306-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see AA057877). This deletion mutant was used to examine the interaction of MRIT alpha 1 with caspases. The FLICE-P20 domain interacted with MRIT alpha 1 but not with MRIT-D/S. The invention provides multiple isoforms of MRIT (see AA05787-89), isolated active fragments of which have either pro-apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors of MRIT apoptotic activity can be identified and used to treat diseases mediated by the dysfunction of programmed cell death or proliferation, such as cancer or a neurodegenerative disorder. Note: the present sequence is not shown in the specification but is derived from the MRIT alpha 1 sequence given in figure 1F

XX Sequence 175 AA;
SQ

Query Match 37.9%; Score 683; DB 2; Length 175;
Best Local Similarity 99.2%; Pred. No. 4.6e-60;
Matches 129; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 192 DSFPCVVSRSQSVYGVDPQTHSGPLHRIHFMFGDSOPYLAKGPKKFFIIONVVGSG 251
DB 1 DSFPCVVSRSQSVYGVDPQTHSGPLHRIHFMFGDSOPYLAKGPKKFFIIONVVGSG 60
QY 252 QLEDSLLLEVDPAMKVEFKAKRGGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQ 311
DB 61 QLEDSLLLEVDPAMKVEFKAKRGGLCTVHREADFFWSLCTADMSLLEQSHSSPSLYLQ 120
QY 312 CLSQKLRQER 321
DB 121 CLSQKLRQER 130

RESULT 8

AAE26110

ID AAE26110 standard; protein: 270 AA.
XX AC AAE26110;

XX 14-NOV-2002 (first entry)

XX Human FLAME-1b protein.

XX Human FLAME-1b protein.

XX Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
XX Gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
XX FLAME-1b.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 227..270

XX /note="FLAME-1b unique region"

XX US2002086983-A1.

XX 04-JUL-2002.

XX 22-AUG-2001; 2001US-00935223.

XX 28-OCT-1997; 97US-00959167.

XX 26-MAR-1999; 99US-00276993.

XX 28-NOV-2000; 2000US-00723450.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;
XX WPI; 2002-642259/69.

XX Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
XX apoptosis, treating diseases characterized by apoptosis e.g. HIV
XX infection and Alzheimer's disease, and for identifying modulators of the
XX protein.

XX Example; Fig 1a; 35pp; English.

The invention relates to FADD-like apoptotic/anti-apoptotic proteins
CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME
CC sequences are useful for inhibiting apoptosis and for gene therapy of
CC diseases characterised by apoptosis including HIV infection and
CC Alzheimer's disease. FLAME inhibitors are useful as apoptotic agents and
CC activators are useful as anti-apoptotic agents. FLAME-1 is useful as a
CC substrate for caspase in assays to identify caspase inhibitors. The
CC present sequence is human FLAME-1b protein

XX Sequence 270 AA;
SQ

Query Match 36.8%; Score 661.5; DB 5; Length 270;
Best Local Similarity 88.8%; Pred. No. 1.3e-57;
Matches 135; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKTSKESKFLDLVVELEKLNIVAPDQLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKTSKESKFLDLVVELEKLNIVAPDQLDLEKCL 156
QY 61 KNTHRIDLKTIKYQSVQAGTSTRNTLQAALQKSLKDPENNFRREPVKKSIQESNAF 120
DB 157 KNTHRIDLKTIKYQSVQAGTSTRNTLQAALQKSLKDPENNFRREPVKKSIQESNAF 202
QY 121 LPQSIPEERYKMSKPLGICLIIDICGNTEL 152
DB 203 ---SIPBERYKMSKPLGICLIIDICGNTEL 231

RESULT 9

AA05795
ID AA05795 standard; protein: 227 AA.
XX

```

AC AAY05795;
XX
XX 02-AUG-1999 (first entry)
DT
XX
XX MRIT beta 2 polypeptide.
DE
XX
XX MRIT beta 2; MACH related inducer of toxicity; human; apoptosis;
XX anti-apoptotic; cancer; autoimmune disease; angiogenesis;
XX atherosclerosis; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
XX aplastic anaemia; myocardial infarction; therapy; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO9918230-A2.
XX
XX 15-APR-1999.
XX
XX 07-OCT-1998; 98WO-US021132.
XX
XX 07-OCT-1997; 97US-00946226.
XX
XX (UNITIV) UNIV. WASHINGTON.
XX
XX Chaudhary FM;
XX
XX WPI; 1999-277275/23.
XX
XX Identifying regulators of MACH-related inducer of toxicity.
XX
XX Example 2; Page; 78pp; English.
XX
XX The present sequence represents MRIT beta 2, comprising amino acid
XX residues 1-227 of novel human MACH-related inducer of toxicity MRIT alpha
XX 1 (see AAY05787). This deletion mutant was used to examine the
XX interaction of MRIT alpha 1 with caspases. The results indicated that the
XX C-terminal 216 residues of MRIT are not sufficient for FLICE-P20
XX interaction. The invention provides multiple isoforms of MRIT (see
XX AAY05787-89), isolated active fragments of which have either pro-
XX apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
XX of MRIT apoptotic activity can be identified and used to treat diseases
XX mediated by the dysfunction of programmed cell death or proliferation,
XX such as cancer or a neurodegenerative disorder. Note: the present
XX sequence is not shown in the specification but is derived from the MRIT
XX alpha 1 sequence given in figure 1F
XX
XX Sequence 227 AA:
SQ
Query Match 30.0%; Score 540; DB 2; Length 227;
Best Local Similarity 85.5%; Pred. No. 1.6e-45;
Matches 112; Conservative 1; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGDLDSKSVSSLIPLMKDYMGKISKESKESFLDLVLEKLNVAPODLLEKCL 60
DB 97 MAEIGDLDSKSVSSLIPLMKDYMGKISKESKESFLDLVLEKLNVAPODLLEKCL 156
QY 61 KNHRIIDLKTKIQTKYKOSVQAGTSYRNVLCQAIOKSLKDPSSNNFR----- 106
DB 157 KNHRIIDLKTKIQTKYKOSVQAGTSYRNVLCQAIOKSLKDPSSNNFRILHNGRSKEQRLKEQ 216
QY 107 ----EEPVKKS 113
DB 217 LGAQGEVPVKKS 227

```

```

XX
XX Human G1 protein isoform beta (CASH-beta).
DE
XX
XX G1 protein; CASH-beta; human; caspase homologue; Fas receptor; modulator;
XX apoptosis; cell death; inflammation; tumour; HIV; therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Domain 2..73
XX /note="death domain/MORT module"
XX Domain 93..142
XX /note="death domain/MORT module"
XX
XX WO9839435-A1.
XX
XX 11-SEP-1998.
XX
XX 26-FEB-1998; 98WO-IL000098.
XX
XX 03-MAR-1997; 97IL-00120367.
XX 01-MAY-1997; 97IL-00120759.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX Wallach D, Goltsev Y, Kovalenko A, Varfolomeev E, Brodianski V;
XX WPI; 1998-495842/42.
XX
XX N-PSDB; AAV52969.
XX
XX New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate
XX the effects of Fas and tumour necrosis factor receptors, useful for
XX killing of cells e.g. HIV and cancer cells.
XX
XX Claim 13; Fig 2; 13pp; English.
XX
XX This is the amino acid sequence of the beta isoform of novel human G1
XX protein. The sequence is deduced from an isolated skin fibroblast cDNA
XX clone (see AAV52969). G1-beta (also called CASH beta, CASH being caspase
XX homologue) and a longer isoform, G1-alpha (see AAV78903), represent 2
XX splice variants of the G1 protein. These G1 proteins are capable of
XX binding to, or interacting directly or indirectly, via their N-terminal
XX MORT modules, with MORT-1 or with MORT-binding proteins such as Mch4
XX (CASP-10) and MACH (CASP-8), and thereby of binding to the intracellular
XX domain of the Fas-R receptor, to which MORT-1 binds, or of binding to the
XX intracellular domain of the p55 tumour necrosis factor (TNF) receptor, to
XX which TRADD binds and to which TRADD protein MORT-1 binds. Hence, they
XX are considered as mediators or modulators of Fas-R having a role in e.g.
XX the signalling process that is initiated by the binding of Fas ligand to
XX Fas-R, and also having a role in the signalling process initiated by the
XX binding of TNF to p55-R. The longer isoform also has a C-terminal caspase
XX active region involved in cytotoxic activity. G1 DNA (I) and
XX polypeptide (II), vectors and fragments are used to regulate cell death
XX or inflammatory processes. (II) is used to inhibit cell death, and its
XX inhibitors augment/enhance the processes. (I) and (II) regulate the Fas-R
XX ligand or TNF effect on cells carrying an Fas-R or p55-R. Tumour, HIV-
XX infected or other diseased cells can be treated using a viral vector
XX encoding a viral surface protein, which binds a specific cell surface
XX receptor and a sequence encoding (II), which kills the cell. Antisense
XX oligonucleotides, introduced using the above vector, block the expression
XX of (II) and can also regulate the above effects. These effects can also
XX be regulated using a vector encoding a ribozyme that interacts with a
XX cellular mRNA encoding (II), and allows (II) expression
XX
XX Sequence 221 AA:
SQ
Query Match 29.3%; Score 527; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGDLDSKSVSSLIPLMKDYMGKISKESKESFLDLVLEKLNVAPODLLEKCL 60
DB 97 MAEIGDLDSKSVSSLIPLMKDYMGKISKESKESFLDLVLEKLNVAPODLLEKCL 156

```

QY 61 KNHRIDLTKTKIOKYKQSVQAGTSTRNVLOAIIQKSLKDPSSNNR 106
 DB 157 KNHRIDLTKTKIOKYKQSVQAGTSTRNVLOAIIQKSLKDPSSNNR 202

RESULT 11
 ID AAM76630 standard; protein; 221 AA.

AC AAM76630;
 DT 12-JUL-1999 (first entry)
 DE Human CFLIP-S protein.
 KW Death effector domain; human; murine; anti-apoptotic; treatment;
 KW HIV infection; autoimmune disease; FLIP protein.

OS Homo sapiens.
 PN DE19713393-A1.
 PD 08-OCT-1998.
 PF 01-APR-1997; 97DE-01013393.
 PR 01-APR-1997; 97DE-01013393.

XX (TSCH/) TSCHOPP J.
 XX Tschoopp J, Thome M, Burns K, Irmeler M, Hahne M, Schroeter M;
 PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;
 DR WPI: 1998-532710/46.
 DR N-PSDB; AAV61936.

XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
 PT infections and autoimmune diseases.
 PS Claim 20; Fig 4A; 45pp; German.

CC This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases

XX Sequence 221 AA;

Query Match 29.3%; Score 527; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.2e-44;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSPFLDVVELEKINLVAPDQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSPFLDVVELEKINLVAPDQDLLEKCL 156
 QY 61 KNHRIDLTKTKIOKYKQSVQAGTSTRNVLOAIIQKSLKDPSSNNR 106
 DB 157 KNHRIDLTKTKIOKYKQSVQAGTSTRNVLOAIIQKSLKDPSSNNR 202

RESULT 12
 ID AAY05789 standard; protein; 221 AA.

AC AAY05789;
 DT 02-AUG-1999 (first entry)

XX Human MACH related inducer of toxicity WRIT beta 1.
 XX WRIT beta 1; MACH related inducer of toxicity; human; apoptosis;

KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
 KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
 KW aplastic anaemia; myocardial infarction; therapy.

OS Homo sapiens.
 PN W09918230-A2.
 PD 15-APR-1999.
 PF 07-OCT-1998; 98WO-US021132.
 PR 07-OCT-1997; 97US-00946226.

XX (UNIW) UNIV WASHINGTON.
 XX Chaudhary PM;
 DR WPI: 1999-277275/23.
 DR N-PSDB; AAX25510.

PT Identifying regulators of MACH-related inducer of toxicity.
 PS Example 1; Fig 1H; 78pp; English.

XX The present sequence represents novel human MACH-related inducer of
 CC toxicity (WRIT) isoform WRIT beta 1, a CED-4 homologue. Multiple isoforms
 CC of WRIT have been identified, some of which function to induce caspase
 CC dependent apoptosis in mammalian cells, e.g. WRIT alpha 1 (see AAY05787)
 CC and WRIT beta 1, while others have anti-apoptotic activity, e.g. WRIT
 CC alpha 2 (see AAY05788). WRIT beta 1 lacks the N-terminal death effector
 CC domain of WRIT alpha 1 but includes a C-terminal caspase ICE homology
 CC domain region. Selective enhancers and inhibitors of WRIT apoptotic
 CC activity can be identified and used to treat diseases mediated by the
 CC dysfunction of programmed cell death or proliferation. A cell
 CC accumulation disorder such as cancer, autoimmune disease, viral
 CC infection, angiogenesis or atherosclerosis is created by administering an
 CC agent that selectively enhances WRIT apoptotic activity, thereby inducing
 CC apoptosis in a subject. A disorder of cell loss, such as a
 CC neurodegenerative disorder, including Alzheimer's disease, Parkinson's
 CC disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
 CC infarction or AIDS can be treated by administering an agent that
 CC selectively inhibits WRIT apoptotic activity

XX Sequence 221 AA;

Query Match 29.3%; Score 527; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3.2e-44;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSPFLDVVELEKINLVAPDQDLLEKCL 60
 DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSPFLDVVELEKINLVAPDQDLLEKCL 156
 QY 61 KNHRIDLTKTKIOKYKQSVQAGTSTRNVLOAIIQKSLKDPSSNNR 106
 DB 157 KNHRIDLTKTKIOKYKQSVQAGTSTRNVLOAIIQKSLKDPSSNNR 202

RESULT 13
 ID AAY57455 standard; protein; 221 AA.

AC AAY57455;
 DT 25-FEB-2000 (first entry)

XX Human FLICE-like inhibitory protein short form protein sequence.
 DE Human FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
 KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
 KW atherosclerosis; vascular wall inflammation; vascular injury;

KW	Fas ligand-mediated apoptosis; atherosclerosis; transplant.
XX	Homo sapiens.
OS	
XX	MO9942570-AI.
FN	
XX	26-AUG-1999.
PD	
PF	19-FEB-1999; 99MO-US003558.
PR	20-FEB-1998; 98US-0075471P.
XX	(SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
PA	
XX	Walsh K;
PI	
DR	NPI; 1999-527469/44.
DR	N-PDSB; AA239041.
XX	Treating conditions characterized by vascular wall inflammation.
PT	
XX	Example 2; Page 72; 105pp; English.
PS	
XX	The present sequence represents human FLICE-like inhibitory protein short form, designated FLIP-S. The present invention describes a new treatment of a condition characterised by vascular wall inflammation in a subject comprising administering a FLIP molecule to inhibit Fas ligand-mediated apoptosis of vascular endothelial cells in the subject. The method can be used to treat atherosclerosis, transplant arteriosclerosis and vascular injury
CC	
CC	
CO	Sequence 221 AA;
SQ	
Query Match	29.3%; Score 527; DB 2; Length 221;
Best Local Similarity	100.0%; Pred. No. 3.2e-44;
Matches	106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MAETGDDLDKSDVSSLLFLMKDYMGKGKISKESFDDLVALEKLNIVAPDQLDLIEKCL 60
DB	97 MAEIGEDLDKSDVSSLLFLMKDYMGKGKISKESFPDLVALEKLNIVAPDQLDLIEKCL 156
OY	61 KNHRIIDLKTKEIKKYKQSYOGAGTSRYNVLDAALQKSFKDPNNFR 106
DB	157 KNHRIIDLKTKEIKKYKQSYOGAGTSRYNVLDAALQKSLKDPNNFR 202
RESULT 14	
ID	AAB03959 standard; protein; 221 AA.
AA	AAB03959
XX	
AC	AAB03959;
XX	
DT	26-FEB-2001 (first entry)
XX	
DE	FLICE-like inhibitor protein (Genbank Accession No. 2253681).
XX	
KW	Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP;
RBS	TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW	tumour specific antigen; immune response; therapy; prophylaxis;
KW	diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW	acquired immune deficiency syndrome; human.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FN	WO200059935-A1.
XX	
PD	12-OCT-2000.
XX	
PF	05-APR-2000; 2000MO-US009002.
XX	
PR	05-APR-1999; 99US-0127867P.
PR	06-APR-1999; 99US-0128021P.
ER	

XX	(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA	(PAPA C) PAPA C
RA	(ALGE/) ALGECIRAS-SCHMINICH A.
PI	Paya C, Algeciras-Schminich A;
XX	
DR	WPJ; 2000-66498/64.
XX	
PT	Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
FT	comprises portion of anti-apoptotic polypeptide linked to a transport
PT	group.
PS	
XX	
XX	Disclosure; Page 78-79; 89pp; English.
CC	A chimeric group or fusion peptide which comprises a portion of an anti-
CC	apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC	combination with a transport group is described. The transport group is
CC	capable of transporting the chimeric group or fusion peptide across the
CC	cell membrane. The anti-apoptotic polypeptide is Fltce-like inhibitor
CC	protein (Flitp) which inhibits Fas and TNF mediated apoptosis by
CC	inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC	shutting off the downstream Fas signalling pathway. The chimeric group
CC	and fusion peptide are useful for inhibiting ligand-induced apoptosis by
CC	bringing them into contact with T cells. The chimeric group is useful for
CC	expanding T cells in vitro e.g. T cells specific for particular antigens
CC	such as tumour-specific antigen, for enhancing immune response and to
CC	inhibit the apoptosis of chronically activated T cells e.g. activated
CC	CD4 ⁺ T cells in HIV infected patients. The chimeric group is also useful
CC	for therapeutic, prophylactic or diagnosis of intracellular delivery of
CC	small molecules and macromolecules such as anti-apoptotic polypeptides
CC	and nucleic acids encoding such polypeptides
SQ	
XX	Sequence 221 AA;
XX	
Query Match	29.3%; Score 527; DB 3; Length 221;
Best Local Similarity	100.0%; Pred. No 3,2e+44;
Matches 106; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 MEIGEDLDKDVSSLLIFMKDYMGRGISKEKSFLDLVLEELKNLVAAPDQLILEKCL 60
DB	97 MAEIGEDLDKSPVSSLIFMKDYMGKGISKEKSFLDLVLEELKNLVAAPDQLILEKCL 156
QY	61 KNHRIIDLTKTIQKYKOSVGAGSYNNYLQAALQKSLKPNNFR 106
DB	157 KNHRIIDLTKTIQKYKOSVGAGSYNNYLQAALQKSLKPNNFR 202
RESULT 15	
ID	AAB61117
XX	AAB61117 standard; protein; 221 AA.
AC	
XX	AAB61117;
DT	02-MAY-2001 (first entry)
DE	
XX	Human MRITAlpha.
XX	
KW	Human; MRITAlpha; apoptotic; nuclear factor-kappa B, NF-kB,
XX	Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant.
OS	
XX	Homo sapiens.
FN	
XX	US6160035-A.
PD	
XX	12-DEC-2000.
PF	
XX	24-AUG-1999; 99US-00382155.
PR	
XX	07-MAY-1996; 98US-00074044.
PA	(UNIV) UNIV WASHINGTON
PA	(STOM-) STOMERS INST MEDICAL RES.

XX Hood L, Chaudhary PM;
PI
XX
DR MPI; 2001-101569/11.
XX
PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
PT for therapeutic purposes.
XX
PS Example 8; Col 43-46; 60pp; English.
XX
CC The present sequence has been shown to regulate the nuclear factor-kappa
CC B (NF-kB), Jun N-terminal kinase (JNK) and apoptosis pathways. It is
CC provided in a specification relating to novel mutants (D73A, L74A and
CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JNK and
CC apoptosis activities. The Caspase-8 mutants are useful for therapeutic
CC purposes and in test methods or assays for determining whether a
CC candidate compound has a significant effect upon cell activities,
CC especially NF-kB, JNK and apoptosis, so as to facilitate the discovery
CC and/or design of therapeutic agents
XX
SQ Sequence 221 AA;

Query Match 29.3%; Score 527; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGDDLDKSDVSSLIFLMKDYMGKISKEKSFLLVVELEKLNVAPOQLLEKCL 60
DB 97 MAEIGDDLDKSDVSSLIFLMKDYMGKISKEKSFLLVVELEKLNVAPOQLLEKCL 156
QY 61 KNHRIIDLKTKIQKYSVGGAGTSYRNVLQAAIQKSLKDPNNFR 106
DB 157 KNHRIIDLKTKIQKYSVGGAGTSYRNVLQAAIQKSLKDPNNFR 202

Search completed: September 8, 2004, 06:24:38
Job time : 132 secs

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REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-6

Query Match 100.0%; Score 1800; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.1e-170;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
DB 1 MAEIGEDLDKSDVSSLIIFLMKDYMRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
QY 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFREEPVKKSIOSEAF 120
DB 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFREEPVKKSIOSEAF 120
QY 121 LPOSIPERIRYKMSKPLGICLIIDCIGNETELRDFTSLGYEVQKFLHLSMHGISQILG 180
DB 121 LPOSIPERIRYKMSKPLGICLIIDCIGNETELRDFTSLGYEVQKFLHLSMHGISQILG 180
QY 181 QFACMPERHDYDSFVCVLVSRGSGSVYGVDTQHSGLPLHIRMFMGDSCEPLAGKPRM 240
DB 181 QFACMPERHDYDSFVCVLVSRGSGSVYGVDTQHSGLPLHIRMFMGDSCEPLAGKPRM 240
QY 241 PFIONVYVSDQLEDSSLEVDGPAKNVEFKAQKRGCLCTVHREADFFWMSLCTADMSLLE 300
DB 241 PFIONVYVSDQLEDSSLEVDGPAKNVEFKAQKRGCLCTVHREADFFWMSLCTADMSLLE 300
QY 301 QSHSPSLYLOCLSQKLRQERGTIPGSGITTESKDMHFSLSGCLLDVL 348
DB 301 QSHSPSLYLOCLSQKLRQERGTIPGSGITTESKDMHFSLSGCLLDVL 348

RESULT 2
US-10-713-208-6
; Sequence 6, Application US/10713208
; Publication No. US20040121387A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 an
; FILE REFERENCE: PF381C1D1
; CURRENT APPLICATION NUMBER: US/10713,208
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 09/489,155
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-208-6
Query Match 100.0%; Score 1800; DB 16; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.1e-170;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60

DB 1 MAEIGEDLDKSDVSSLIIFLMKDYMRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
QY 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFREEPVKKSIOSEAF 120
DB 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFREEPVKKSIOSEAF 120
QY 121 LPOSIPERIRYKMSKPLGICLIIDCIGNETELRDFTSLGYEVQKFLHLSMHGISQILG 180
DB 121 LPOSIPERIRYKMSKPLGICLIIDCIGNETELRDFTSLGYEVQKFLHLSMHGISQILG 180
QY 181 QFACMPERHDYDSFVCVLVSRGSGSVYGVDTQHSGLPLHIRMFMGDSCEPLAGKPRM 240
DB 181 QFACMPERHDYDSFVCVLVSRGSGSVYGVDTQHSGLPLHIRMFMGDSCEPLAGKPRM 240
QY 241 PFIONVYVSDQLEDSSLEVDGPAKNVEFKAQKRGCLCTVHREADFFWMSLCTADMSLLE 300
DB 241 PFIONVYVSDQLEDSSLEVDGPAKNVEFKAQKRGCLCTVHREADFFWMSLCTADMSLLE 300
QY 301 QSHSPSLYLOCLSQKLRQERGTIPGSGITTESKDMHFSLSGCLLDVL 348
DB 301 QSHSPSLYLOCLSQKLRQERGTIPGSGITTESKDMHFSLSGCLLDVL 348

RESULT 3
US-09-410-194-15
; Sequence 15, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imbler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroeter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, B. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-15
Query Match 29.3%; Score 527; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 8.3e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMRGKISKESFLDLVVELEKLNVAAPDQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFREEPVKKSIOSEAF 106
DB 157 KNHRIIDLTKTKIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFREEPVKKSIOSEAF 202
RESULT 4
US-09-410-194-22
; Sequence 22, Application US/09410194


```
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: Teschopp, Jung
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Imbler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-410-194-22

Query Match      29.3%; Score 527; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 8.3e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  MAEIGELDSDVSSLIPLMKDYMGRGKISKESKSPDLVVELEKLNIVAPDLDLEKCL 60
Db      97  MARIGEDLDSDVSSLIPLMKDYMGRGKISKESKSPDLVVELEKLNIVAPDLDLEKCL 156

Oy      61  KNIRHIDLKTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPSSNFR 106
Db      157 KNIRHIDLKTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPSSNFR 202

RESULT 5
US-09-864-761-35073
Sequence 35073, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263, 6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35073
LENGTH: 76
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007283.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.9
OTHER INFORMATION: EST_HUMAN HIT: A1139524.1, EVALU2 2.00e-38
US-09-864-761-35073

Query Match      21.7%; Score 391; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 5.7e-31;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      245  NYVVSQGLEDSLLVDDPAMKNVEFKQKRGCTVHREADFESLCTADMSLJEQSHS 304
Db      1  NYVVSQGLEDSLLVDDPAMKNVEFKQKRGCTVHREADFESLCTADMSLJEQSHS 60

Oy      305  SPSLYIQCLSQKLRQE 320
Db      61  SPSLYIQCLSQKLRQE 76

RESULT 6
US-10-627-571-5
Sequence 5, Application US/10627571
Publication No. US20040082771A1
GENERAL INFORMATION:
APPLICANT: KASID, Usha N.
APPLICANT: KUMAR, Deepak
APPLICANT: GOKHALE, Pritulula
APPLICANT: AHYAD, Imran
TITLE OF INVENTION: ANTI-APOTOTIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
FILE REFERENCE: 223316
CURRENT APPLICATION NUMBER: US/10/627,571
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 25
```

SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: CASH Alpha/Beta - fragment
US-10-627-571-5

Query Match 15.4%; Score 277; DB 16; Length 56;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 66
DB 1 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 56

RESULT 7
US-10-627-571-7
Sequence 7, Application US/10627571
Publication No. US20040082771A1
GENERAL INFORMATION:
APPLICANT: KASID, Usha N.
APPLICANT: KUMAR, Deepak
APPLICANT: GOKHALE, Prafulla
APPLICANT: AHMAD, Imran
TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USAS
FILE REFERENCE: 22316
CURRENT APPLICATION NUMBER: US/10/627,571
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: MISC FEATURE
NAME/KEY: MISC FEATURE
OTHER INFORMATION: FLIP (L) - fragment
US-10-627-571-7

Query Match 15.4%; Score 277; DB 16; Length 56;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 66
DB 1 SDVSSLIPLMKDYMGRGKISKEKSFLLVLELEKLNIVAPDQDLLEKCKLNHRI 56

RESULT 8
US-10-368-438-16
Sequence 16, Application US/10368438
Publication No. US20030219411A1
GENERAL INFORMATION:
APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya V. GONCHAROV
Tanya V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Broadway and Newmark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/368,438
FILING DATE: 20-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Broadway, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-368-438-16

Query Match 14.5%; Score 261.5; DB 15; Length 335;
Best Local Similarity 26.6%; Pred. No. 4.2e-17;
Matches 86; Conservative 60; Mismatches 108; Indels 69; Gaps 13;

QY 28 KISKESKFLVLELEKLNIVAPDQDLLEKCKLNHRIIDLTXTQYKQSGVQAGSYR 87
DB 3 KLDDDMNLDFLEMEKRVILGEGKIDILVCAQINSLKI-INDYBSKSEELC-- 59
QY 88 NVLOALQKSLKDPNSNFFREBPYKSIQSEAFLLPQSIPEERYKXKXPLGICIIIDIG 147
DB 60 -----GWMITISPRE-----QSES---QTL-DKYQKSKPRGVCIIINHN 99
QY 148 -----NETEL-----LNDTFSIGYEVQKFLHLSMHSQISQIGFACMP 186
DB 100 FAYAREKVPKLSIRDRNGTHLDAGALITTFEELHFEIRPHDDCTVEQIYEIWKIYQLM- 158
QY 187 EHRDYDSFVCVLVSRGSGOSVYGVDTGTHGLPLHIRMFMGDSCTYLAGKXMPFIQ-- 244
DB 159 DHNMOCFLICLISHDKGIITGTGQEG--PIYELTQFTGLKCPSLAGKPKVFFIAC 216
QY 245 ---NY---VYSQGLDSSLSLEVD--GPMKQVVERKQKRGICLTHRADPFWISCTADM 296
DB 217 QGDNYKGIPIVEDSEOPYLEMDLSSPOTRYIP-----DEADFLGATVNN 264
QY 297 SLLEQSHSPSYLQCTSQKRO 319
DB 265 CVGYRNPAGETWYIGSLQSLRE 287

RESULT 9

RESULT 15
US-10-171-077-5
Sequence 5, Application US/10171077
Publication No. US20030022353A1

GENERAL INFORMATION:

APPLICANT: Litwack, Gerald
Alnemri, Emdad S.
Fernandez-Alnemri, Teresa
TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE
PROTEASE,
AND COMPOSITIONS FOR MAKING AND
METHODS

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
No. US20030022353A1r1s

STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/171,077
FILING DATE: 12-Jun-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,925
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1508

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-171-077-5
Query Match 11.1%; Score 199; DB 14; Length 293;
Best Local Similarity 27.5%; Pred. No. 5,7e-11;
Matches 69; Conservative 33; Mismatches 75; Indels 74; Gaps 10;

QY 111 KKSIOSEAPLPQSI--PEERYKSKRPGLICLIID-----CIGNETEL 152
DB 16 EENMTETDAFYKREMPDAEKYKMDHRRGIALIFNHERFFWLTLPERRRCADRDN-- 73
QY 153 LADFTSLGCVGQKE-----LHLSMHGTSQILGQFACMPEHRDYSFYCVLVSRGSSQ 205
DB 74 LTRRRPSDLGFEVVKCFNDIKAEELILKIHVESTV-----SHADADCFVCFVLSHGEEN 125
QY 206 SVYGVYD-----QTSGLPLHHRIRMFMDSCPYLAGKPKMFPIQ-----NYVY 248
DB 126 HIYAVDAKIEIQTLTGL-----FKGDKCHSLVAKPKIFIIQACRGNQHDVPVPIPLDV 177
QY 249 SDGQLE--DSSLLEVDGAMKGVKFAQKRGKGLCTVREADFFWMSLCTADKSLLEQSHSSP 306
DB 178 VDNQTEKLDITNITEVDAS-----VYTLPAAGADFLMCYSVAEGYVSHRETVNG 225
QY 307 SVYLOCSQKL 317
DB 226 SWYIDLCENL 236

Search completed: September 8, 2004, 06:37:53
Job time : 128 secs

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